

	CAGGAGGGCG AGKGTTCGTG GGCTCCCATC TKAAC TGACA AACTCATGAT GGACGGCCAC	360
5	GAGGTGACCG TGGTGGACAA TTTCTTCACG GGCAGGAAGA GAAACGTGGA GCACTGGATC	420
	GGACATGAGA ACTTCGAGTT GATTAACCAC GACGTGTGGG AGCCCCCTCTA CATCGAGGTT	480
	GACCAGATAT ACCATCTGGC ATCTCCAGCC TCCCCCTCAA ACTACATGTA TAATCCTATC	540
10	AAGACATTAA AGACCAATAC GATTGGGACA TTAAACATGT TGGGGCTGGC AAAACGAGTC	600
	GGTGCCCGTC TGCTCCTGGC CTCCACATCG GAGGTGTATG GAGATCCTGA AGTCCACCCT	660
15	CAAAGTGAGG ATTACTGGGG CCACGTGAAT CCAATAGGAC CTCGGGCCTG CTACGATGAA	720
	GGCAAACGTG TTGCAGAGAC CATGTGCTAT GCCTACATGA AGCAGGAAGG CGTGAAGTGT	780
	CGAGTGCCCA GAATCTTCAA CACCTTTGGG CCACGCATGC ACATGAACGA TGGGCGAGTA	840
20	GTCAGCAACT TCATCTGCA GGCCTCCAG GGGGAGCCAC TCACGGTATA CGGATCCGGG	900
	TCTCAGACAA GGGCGTTCCA GTACGTCAGC GATCTAGTGA ATGGCCTCGT GGCTCTCATG	960
25	AACAGCAACG TCAGCAGCCC GGTCAACCTG GGGAAACCCAG AAGAACACAC AATCCTAGAA	1020
	TTTGCTCAGT TAATTAAAAA CCTTGTGGT AGCGGAAGTG AAATTCAAGT TCTCTCCGAA	1080
	GCCCAGGATG ACCCAGAGAA AAGAAAACCA GACATCAAAA AAGCAAAGCT GATGCTGGGG	1140
30	TGGGAGCCCG TGGTCCCGCT GGAGGAAGGT TTAAACAAAG CAATTCACTA CTTCCGTAAA	1200
	GAACTCGAGT ACCAGGCAAA TAATCAGTAC ATCCCCAAC CAAAGCTGC CAGAATAAAG	1260
35	AAAGGACGGA CTCGCCACAG CTGAACTCCT CACTTTTAGG ACACAAGACT ACCATTGTAC	1320
	ACTTGATGGG ATGTATTTTT GGCTTTTTTT TGTGTGCTT TAAAGAAAGA CTTTAACAGG	1380
	TGTCATGAAG AACAACTGG AATTTTCATC TGAAGCTTC TTTAATGAAA TGGATGTGCC	1440
40	TAAAAGCTCC CCTCAAAAA CTGCAGATTT TGCCTGCAC TTTTGAATC TCTCTTTTTA	1500
	TGTAAATAG CGTAGATGCA TCTCTGCGTA TTTTCAAGTT TTTTATCTT GCTGTGAGAG	1560
45	CATATGTGT GACTGTCGTT GACAGTTTITA TTTACTGGTT TCTTTGIGAA GCTGAAAAGG	1620
	AACATTAAGC GGGACAAAA ATGCCGATTT TATTTATAAA AGTGGGTACT TAATAAATGA	1680
	GTCGTTATAC TATGCATAAA GAAAAAYCCT AGCAGTATTG TCAGGTGGTG GTGCGCCGGC	1740
50	ATTGATTTTA GGCAGATAA AAGAATTCTG TGTGAGAGCT TTATGTTTCT CTTTAAATTC	1800
	AGAGTTTTTC CAAGGTCTAC TTTTGAGTTG CAAACTTGAC TTTGAAATAT TCCTGTTGGT	1860
55	CATGATCAAG GATATTTGAA ATCACTACTG TGTTTTGCTG CGTATCTGGG GCGGGGGCAG	1920
	GTTGGGGGGC ACAAAGTTAA CATATTCTTG GTTAACCATG GTTAAATATG CTATTTTAAT	1980
	AAAATAATGA	1990

## (2) INFORMATION FOR SEQ ID NO: 276:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2436 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

	AACCTCGCTT AGCTCTCCAG GGTNAACGG GTGAGNCCTT AAAAACAGAA GAGAACAAGA	60
15	TTTAAAGTCC GTTGCATTGA AAATAACAAA CAATATCAAT GTTTTAATCA AGGATCTCTT	120
	CCACATTCTT CCTTCTTATA AGAGCACAGT AACACTATCC TGGAAACCTG TACAAAAGGT	180
	TGAGATTGGG CAAAAGAGAG CCAGTGAAGA TACAACTTCA GGTTCACCAC CCAAGAAATC	240
20	TTCAGCAGGA CAAAAAGAG ATGCCAGGCA GATTTATAAC CCTCCCAGTG GGAAATATAG	300
	CAGCAATTTG GGCAACTTTA ATTATGAGCA GAGAGGAGCC TTCAGGGGAA GTAGAGGTGG	360
25	CCGAGGTGGG GGCACACGAG GAAATCGTAG TCGGGGAAGA CTCTACTGAA TAAGACATCA	420
	GCATTCTTCA GCATGTGCAT GAGCTTAATA TACTTAAATT CTACTACTCA TTGGATTGCC	480
	GGGATGTGCC CTTTAAACAG ACTGCTGCCT TCAGCTAAAA ACTTAATGTT CTTTATACCT	540
30	TTGTATGTAT GACCTACTTT TGTAACAGAC CATGGTTGTG TCCAAGGTAA AACCACAGTG	600
	ATATTTTGGG ATGCTTTGTC TGCAATCTTG ACTTGTTTTT GCAGTATCAT TATTCAGACT	660
35	TCAAATGTG AATCTTTTAA ACATCTTGAT AATTGTGTGT TGAGAGCTGT TCATTCTAAA	720
	ATGTAATGAA ATTCAGTCTA GTTCTGCTGA TAAAGATCAT CAGTTTGTAA AGGTTACTGA	780
	TTTTCTCTTT CCTCTTAGT TTTTACCCTA ATATATGGAG AAGAGTAATG GTCAATCTTA	840
40	ACATTTTGTG TTAATTGTTT AATAAAGCTG CTGGGCAGTG GTGCAGCAAT CCTACCTAGT	900
	GTCATAAAG CAAAATACTT ACATAGCTTT CTTAAAATAT AGGAATGACA TTACATTTTT	960
45	AGGAGAAAGT AAGTTGCTTT GCACCGCTA CTTAATCTT TTCCATATAT TGTGATACAA	1020
	ACTTTTGAAT ATGGAATCTT ACTATTTGAA TAGAAATGTG TATGTATAAT ATACATACAT	1080
	ACATAAGCAT ATATGTGTGT GTGTGTGTGT ATATATATAT ATATGCATGC TGTGAAACTT	1140
50	GACTACACAA CATAAATCAC TTTTAAATT CCAGGAACGG GTAGTCTGAC ACGGTGATTA	1200
	TCCTTTTGAG GCTGAATCCG TTATTAACCT GTTATTTAGG TTTTACTCC CAGTAGCAAG	1260
55	GGATTCTAAG TTAGTTGCAC TTACATGATT ATTGTTATTT AAAACTAAGA ATAAAGGCTG	1320
	CATTTTCAAA GATAAATTGG AATGCTGTT GGTGAAATAA CAACCAAAAT ACTGAATCTG	1380
60	ATGTACATAC AGGTTTCTAC AGGAAGAGAT GGTATAATTT ACAATTTGGA GATTTAATAA	1440

	CCAGGGCTAC CCAGAAAAAG TGA	CTTGATA ACATGGTACC AATAAGTAAG GGATGCTCTC	1500
	TCGGTTTGCT TTTGCCACTT TCAAGATTTT	AACTTCTCAG GTTATTAATC AAAATTATTG	1560
5	TATAAGTTAG CCAATAGAAT TTTTAGGTTA	AAACAACAGA TGGGGGGTTT GTGGAGTGT	1620
	TAATGTCATG GGCATTTTTA GTAGCATAGA	CCCTTTGTTT TGCATTGAA TGTTCGTAT	1680
10	ATTTTGTGTT CACAGTTAAT CTTCCTCCC	CAAGTTTGCT ATTCAAATCA ACTGCCTGAA	1740
	TGACATTCT AGTAGTCTGA TGTATTTTTC	TGAGGAATAG TTTGTGATT CAAATGCAGT	1800
	GTCTTCATTA CCATTACCTC TACACTGCAG	AAGAAGCAAA ACTCCTTTAT TAGAATTACT	1860
15	GCACATGTGT ATGGGGAAAA TAGTTCTGAA	AGGCTAGAAT GATACAAGTG AGCAAAAGTT	1920
	GGTCAGCTTG GCTATGGAGT GGTGGCAATA	ATCTCTAAAC ATTCCAAAAG ACCATGAGCT	1980
20	GAACCTAAAC TCCCTTGGA TCTGAACAAA	GGAATATAAA ATTGCCATTT GAAAAGTGAC	2040
	CAGCTAATCT GGACCTCAGA GATAGATCAG	CCAGTGGCCC AAAGCCATTT CAAGTACAGA	2100
	AATTATAGAG ACTACAGCTA AATAAAATTG	AACATTAAAT ATAATTTTAC CACTTTTGT	2160
25	CTTTATAAGC ATATTTGTAA ACTCAGAACT	GAGCAGAAGT GACTTTACTT TCTCAAGTTT	2220
	GATACTGAGT TGACTGTTC CTATCCCTC	ACCCCTCCCC TTCCCTTTCC TAAGGCAATA	2280
30	GTGCACAACT TAGGTATTT TTGCTTCCGA	ATTTGAATGA AAAACTTAAT GCCATGGATT	2340
	TTTTTCTTTT GCAAGACACC TGTTATCAT	CTTGTTTAAA TGTAAATGTC CCCTTATGCT	2400
	TTTGAAATAA ATTTCTTTT GTAATTTTAA	AAAAAA	2436

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(2) INFORMATION FOR SEQ ID NO: 277:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 782 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

	GCCACTGACT TCTCCACCC TTCTGTCTCC	CCCATAATAG TTTATTTGGT TGGTCTGGAC	60
50	TCACTTGTTG CCTTTRATTA AATTCCTAAG	GGGCTGAAG AAGACATTT TACTGCAGAG	120
	GGTTAGAGGC ACTTGAGCAA GGCCCCACA	TCCCAACTCT GGGAGTTGTG GTGGGAGGAG	180
55	GCACCTCTGG GGGATAGGAC CAGACAAGAT	AACAGGAGCT CACATGNNAA GCAGAAGCTG	240
	TGACAAGTTT AGTAGTCCCA AAATGGGTTA	TATCCCTTCC CCCTTACAT CAGAATCTTG	300
	TGAAATGGGA AAACAACAGA AGGAGGGGAT	CAAAGATAGC TGATCTCACA TGCTTCCAG	360
60	GCAGGGCARA GGTGGGAGTC AAACCCGGT	GACAGGTGGG TGGAGAGCCC TGTTTGAGGT	420

5 TGTCGCTGAT CCCTCTCTGG TATTAGTTTT TCCCTGGGA GCAGGAAGCC CTAGGAAGAG 480  
 GGGACTGCAG GGTCCCRGG GGATCTTTC TCCCTCCCT GCATGAGGCA GAGGCAAGCT 540  
 GCCTGCCAAC CCCCTCCCTC AAGGAATGGC CTTGCCCAGG AATGCCACC ACACATACCC 600  
 TCTCTTTTT TTCTAGTCAA ACTCTGTTT ATTCTTGGC TTGCTCCCT CCTTCTCCC 660  
 10 CTCTCAACCT TTAATTCTGA TTCTATTTC ATGGAATTG GGATTGAAGT TAAACTACAA 720  
 CAGTCCGCC AACACCAAGT CTTGCAGGAA AAAAATACAA AGAAATTTAA CAAAAAAAAA 780  
 15 AA 782

20 (2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 961 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

30 GAGTTCCGGC TGGAGACCCG TGCTCTGGG CCGCGCCTTC ACCATGGCCT CGGCAGAGCT 60  
 GGACTACACC ATCGAGATCC CGGATCAGCC CTGCTGGAGC CAGAAGAACA GCCCCAGCCC 120  
 AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC TGTGGTGATT CTYTTGGGCT GGGGTGGCTG 180  
 35 CAAGGACAAG AACCTTGCCA AGTACAGTGC CATCTACCAC AAAAGGGGCT GCATCGTAAT 240  
 CCGATACACA GCCCCGTGGC ACATGGTCTT CTCTCCGAG TCACTGGGTA TCCCTTCACT 300  
 TCGTGTPTTG GCCCAGAAGC TGCTCGAGCT GCTCTTTGAT TATGAGATTG AGAAGGAGCC 360  
 40 CCTGCTCTTC CATGTCTTCA GCAACGGTGG CGTCATGCTG TACCGCTACG TGCTGGAGCT 420  
 CCTGCAGACC CGTCGCTTCT GCCGCCTGCG TGTGGTGGC ACCATCTTTG ACAGCGCTCC 480  
 45 TGGTGACAGC AACCTGGTAG GGGCTCTGCG GGCCCTGGCA GCCATCCTGG AGCGCCGGGC 540  
 CGCCATGCTG CGCCTGTTC TGCTGGTGGC CTTTGCCCTG GTGGTCGTCC TGTTCACGT 600  
 CCTGCTTGCT CCCATCACAG CCTCTTTCCA CACCCACTTC TATGACAGGC TACAGGACGC 660  
 50 GGGCTCTGCG TGGCCCGAGC TCTACCTCTA YTCGAGGGCT GACGAAGTAG TCCTGGCCAG 720  
 AGACATAGAA CGCATGGTGG AGGCACGCCT GGCACGCCG GTCTGGCGC GTTCTGTGGA 780  
 55 TTTGCTGTCA TCTGCACAG TCAGCCACCT CCGTGACTAC CCTACTTACT ACACAAGCCT 840  
 CTGTGTCGAC TTCATGCGCA ACTGCGTCCG CTGCTGAGGC CATTGCTCCA TCTCAMCTCT 900  
 60 GCTCCAGAAA TAAATGCCTG ACAMCTCCCC AAAAAAAAAA AAAAAAAAAA ACTCGAGGGG 960

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961

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(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

20

CGCGCTTTC AGTTCGGTCT CCTGGTGTAC GGCCAACGCC AAGTAGGGGA TTGCGTTCCC	60
TCCAGTCGCA GCCCTATCAG ATTTGGATAT GTCTTCATA TTTGATTGGA TTTACAGTGG	120
TTTCAGCAGT GTGCTACAGT TTTTAGGATT ATATAAGAAA ACTGGTAAAC TGGTATTCT	180
TGGATTGGAT AATGCAGGAA AAACAACATT GCTACACATG CTAAAAGATG ACAGACTTGG	240
ACAACATGTC CCAACATTAC ATCCCACTTC CGAAGAACTG ACCATTGCTG GCATGACGTT	300
TACAACTTTT GATCTGGGTG GACATGTTCA AGCTCGAAGA GTGTGGAAAA ACTACCTTCC	360
TGCTATCAAT GGCATTGTAT TTCTGGTGGG TTGTGCAGAC CACGAAAGGC TGTTAGAGTC	420
AAAAGAAGAA CTTGATTAC TAATGACAGA TGAAACCATT GCTAATGTGC CTATACTGAT	480
TCTTGGGAAT AAGATCGACA GACCTGAAGC CATCAGTGAA GAGAGGTTGC GAGAGATGTT	540
TGGTTTATAT GGTGAGACAA CAGGAAAGGG GAGTATATCT CTGAAAGAAC TGAATGCCCC	600
ACCCTTAGAA GTTTTCATGT GTAGTGTGCT CAAAAGACAA GGTACGGAG AAGGCTTCCG	660
CTGGATGGCA CAGTACATTG ATTAACACAA ACTCACATTG GTTCCAGGTC TCAACGTTCA	720
GGCTTACTCA GAGATTTGAT TGCTCAACAT GCATAACTTG AATTCAATAG ACTTTTGCTG	780
GTTATAAAAC AGATGTTTTT TAGATTATTA ATATTAAATC AACTTAATTT GAATGAGAAT	840
TGAAACTGA TTCAAGTAAG TTTGAGTATC ACAATGTTAG CTTTCTAATT CCATAAAAGT	900
ACTTGGTTTT TACAGTTTAT AATCTGACAT CACCCAGCG CCATTTGTAA AGAGCAACTT	960
TCCAGCAGTA CATTGAAGC ACTTTTAAAC AACATGAAAC TATAAACCAT ATTTAAAGC	1020
TCATCATGTT AAATTTTTTA TGTACTTTTC TGGAAGTAGT TTTTAAATTT TAGATTATAT	1080
GTCCACCTAT CKTAAGTGTA CAGTTAATAA TTAGCTTATT CAATGATTGC ATGATGCCTT	1140
ACAGTTTTC ATAACTTTTT TTCTTATGCA AACGTCATGC AATAAAACAA ACTCTAATGT	1200
TTGGCAAAAA AAAAAAAAAA AAANTCGA	1228

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## (2) INFORMATION FOR SEQ ID NO: 280:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1327 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

10

TCTCGGGTCT CGGACAGGT GAGCACCTG ATGAAGGCCA CGTCCTGAT GCGGCACCTG 60  
GGCGGGTGCA GGAGATCGTG GGCGCCCTCC GCAAGGGCGS CGGAGACCGG TTACAGGTGA 120  
15 TTCTGATTT TRACATGACC TTGAGCAGGT TTGCATATAA TGGAAAGCGA TGCCCTTCTT 180  
CTTACAATAT TCTGATAAT AGCAAGATCA TCAGTGAGGA GTGTGGAAA GAGCTCACAG 240  
CGCTCCTTCA CCACTATTAC CCAATTGAGA TCGACCCACA CCGGACCGTC AAGGAGAAGC 300  
20 TACCTCATAT GGTGGAATGG TGGACCAAAG CGCACAATCT CCTATGTCAG CAGAAGATTC 360  
AGAAGTTTCA GATAGCCCAG GTGGTTAGAG AGTCCAATGC AATGCTCAGG GAGGGATATA 420  
25 AGACCTTCTT CAACACACTC TACCATAACA ACATTCCCCT TTTCATCTTT TCTGCGGGCA 480  
TTGGTGATAT CCTGGAAGAA ATTATCCGAC AGATGAAAGT GTTCCACCCC AACATCCACA 540  
TCGTGTCTAA CTACATGGAT TTTAATGAAG ATGGTTTCTT CCAGGGATTT AAGGGCCAGC 600  
30 TGATACACAC ATACAACAAG AACAGCTCTG TGTGTGAGAA CTGTGGTTAC TTCCAGCAAC 660  
TTGAGGGCAA AACCAATGTC ATCCTGCTGG GAGACTCTAT CGGGACCTC ACCATGGCCG 720  
35 ATGGGGTTCC TGGTGTGCAG AACATTCTCA AAATTGGCTT CCTGAATGAC AAGGTGGAGG 780  
AGCGGCGGGA NCGTAACAT GGACTCCTAT GACATCGTGC TGGAGAAGGA CGAGACTCTG 840  
GATGTGGTCA ACGGGCTACT GCAGCACATC CTGTGCCNAG GGGGTCCAGC TGGAGATGCA 900  
40 AGGCCCCGTA AGGCGCAGGC TCCNAAGKCC SCTGCAGGCC GTGGTGAGGA GGGGCGCCTC 960  
CCCAGAGTCT GCTCCCCCGT GAACACAGAG CAGAGCCAGG GTGGCCAGCA GTGGCTGGGT 1020  
45 CCTTCCGCGC CCTTCCGTCC TCCTTTCCCT GAGCACCTTC ATCACCAGAG GCTTGAAGGA 1080  
ACCCCGCCAT GTGGCAGGGC ACAGGCACTG TTCCTGGTGA ACCTTGGACC ACAGCATGTC 1140  
AGTGCTCTAG GGATGTCTA CTCAGGGAT TTTCTTCAAA ATTTTAAAC ATGGGAAGTT 1200  
50 CAAACAAATA TAATGTGTGA AACAGATCAA AATTTTAAAT ATGAAAAAA AGCTGCTCTG 1260  
ATTACAGGGA TGTGGGTCGG GGTAGAACCT GGACCTCTTG GCCTGGGGGC ACATGGGATG 1320  
55 CTTCTAG 1327

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## (2) INFORMATION FOR SEQ ID NO: 281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

10 TCACCCGTGCC TACAGCGTGG AGCTCAGATG ACTGCGCCCT CCACGGTCAC TGTGAGCAGG 60  
TGGTATTACAG AGCCTGCATG ACCCTCACGG CCAGCCCTGG GGTGTTCCCC GTCAGTGTGT 120  
GGCTTTGGCT GAAGCCTAAT TCCACAGCTC CTTGTTT TTTT GAGAGAGACT GAGAGAACCA 180  
15 TAATCCTTGC CTGCTGAACC CAGCCTGGGC CTGGATGCTC TGTGAATACA TTATCTTGGC 240  
ATGTTGGGTT ATTCCAGCCA AAGACATTTT AAGTGCCTGT AACTGATTGT TACATATTTA 300  
20 TAAAAATCTA TTCAGAAATT GGTCCAATAA TGCACGTGCT TTGCCCTGGG TACAGCCAGA 360  
GCCCTTCAAC CCCACCTTGG ACTTGAGGAC CTACCTGATG GGAGGTTTCC ACGTGTCTCT 420  
AGAGAAGGAT TCCTGGATCT AGCTGGTCAC GACGATGTTT TCACCAAGGT CACAGGAGCA 480  
25 TTGCGTCGCT GATGGGGTTG AAGTTGGTT TGGTTCTTGT TTCAGCCCAA TATGTAGAGA 540  
ACATTTGAAA CAGTCTGCAC CTTTGATACG GTATTGCATT TCCAAAGCCA CCAATCCATT 600  
30 TTGTGGATT TATGTGTCTG TGGCTTAATA ATCATAGTAA CAACAATAAT ACCTTTCTCT 660  
CCATTTTGCT TGCAGGAAAC ATACCTTAAG TTTT TTTT TTTT TTTT TTTT TTTT 720  
TTTGT TTTT CTTTATGAAG AAAAAATAAA ATAGTCACAT TTTTAATACY AAAAAATGGA 780  
35 CAAAAAAGT CGAGGGGG 799

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## (2) INFORMATION FOR SEQ ID NO: 282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

50

AAAGACTCTA ACATCCATGA GCTTGAACAT GAGCAAGAGC CTACTTGTGC CKSCCAGATG 60  
GCTGAGCCCT TCCGTACCTT CCGAGATGGA TGGGTCTCCT ACTACAACCA GCCTGTGTTT 120  
55 CTGGCTGGCA TGGGTCTTGC TTTCTTTTAT ATGACTGTCC TGGGCTTTGA CTGCATCACC 180  
ACAGGGTACG CCTACACTCA GGGACTGAGT GGTTCATCC TCAGTATTTT GATGGGAGCA 240  
TCAGCTATAA CTGGAATAAT GGGAACTGTA GCTTTTACTT GGCTACGTCG AAAATGTGGT 300

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	TTGGTTCCGA CAGGTCTGAT CTCAGGATTG GCACAGCTTT CCTGTTTGAT CTTGTGTGTG	360
	ATCTCTGTAT TCATGCCTGG AAGCCCCCTG GACTTGTCCG TTTCTCCTTT TGAAGATATC	420
5	CGATCAAGGT TCATCAAGG AGAGTCAATT ACACCTACCA AGATACCTGA AATTACAACT	480
	GAAATATACA TGTCTAATGG GTCTAATTCT GCTAATATG TCCCGGAGAC AAGTCCTGAA	540
10	TCTGTGCCCC TAATCTCTGT CAGTCTGCTG TTTGCAGGCG TCATTGCTGC TAGAATCGGT	600
	CTTTGGTCTT TTGATTTAAC TGTGACACAG TTGCTGCAAG AAAATGTAAT TGAATCTGAA	660
	AGAGGCATTA TAAATGGTGT ACAGAACTCC ATGAACTATC TTCTTGATCT TCTGCATTTT	720
15	ATCATGGTCA TCCTGGCTCC AAATCCTGAA GCTTTTGGCT TGCTCGTATT GATTTTCAGTC	780
	TCCTTTGTGG CAATGGGCCA CATTATGTAT TTCCGATTTG CCCAAAATAC TCTGGGAAAC	840
20	AAGCTCTTTG CTTGCGGTCC TGATGCAAAA GAAGTTAGGA AGGAAAATCA AGCAAATACA	900
	TCTGTGTGTT GAGACAGTTT AACTGTGCTT ATCCTGTTAC TAGATTATAT AGAGCACATG	960
	TGCTTATTTT GTACTGCAGA ATTCCAATAA ATGGCTGGGT GTTTTGCTCT GTTTTACCA	1020
25	CAGCTGTGCC TTGAGAACTA AAAGCTGTTT AGGAAACCTA AGTCAGCAGA AATTAACGTA	1080
	TTAATTTCCC TTATGTTGAG GCATGGAAAA AAAATTGGAA AAGAAAACT CAGTTTAAAT	1140
30	ACGGAGACTA TAATGATAAC ACTGAATTCC CCTATTTCTC ATGAGTAGAT ACAATCTTAC	1200
	GTAAAAGAGT GGTAGTCAC GTGAATTCAG TTATCATTTG ACAGATTCTT ATCTGTACTA	1260
	GAATTCAGAT ATGTCAGTTT TCTGCAAAAC TCACTCTTGT TCAAGACTAG CTAATTTATT	1320
35	TTTTTGATC TTAGTTATTT TTA AAAACAA ATTCTTCAAG TATGAAGACT AAATTTTGAT	1380
	AACTAATATT ATCCTTATG ATCCTATGTA TCTTAAGTGA TTTACATGTA TGTGGAAAAA	1440
40	CAAAACACTT AACTAGAATT CTCTAATAAG GTTTATGGTT TAGCTTAAAG AGCACCTTTG	1500
	TATTTTTTATT ATCAGATGGG GCAACATATT GTATGAAGCA TATGTAGCAC TTCACAGCAT	1560
	GGTTATCATG TAAGCTGCAG GTAGAAGCAA AGCTGTAAAG TAGATTTATC ACACAATGAC	1620
45	TGCATACAGA CTTCAAATAT GTCAATAGTT TGGTCATAGA ACCTAGAAGC CAAAAGCCAC	1680
	ACAGAAGGGC AAGAATCCCA ATTAACTCA TGTATCATC ATTAGTGATC TGTGTTGTAG	1740
50	AACATGAGGG TGTAAGCCTT CAGCCTGGCA AGTTACATGT AGAAAGCCCA CACTTGTGAA	1800
	GGTTTGTGTT TACAAATCAC TTGATTTAAC AACTCAGGT AGAATATTTT TATTTTACT	1860
	GTTTTATACC CAGAAGTTAT TTCTACATTG TTCTACAGCA AGAATATTCA TAAAAGTATC	1920
55	CCTTTCAAAT GCCTTTGAGA AGAATAGAAG AAAAAAGTT TGTATATATT TAAAAAATT	1980
	GTTTTAAAAG TCAGTTTGCA ACATGTCGT ACCAAGATGG TACTTTGCCT TAACCGTTTA	2040
60	TATGCACTTT CATGGAGACT GCAATACGTT GCTATGAGCA CTTCTTTTAT CCTTGGAGTT	2100



TAATCCTTTG CTTCACTCTT CTACAGTATG ACATAATGAT TTGCTATGTT GTAAAAATCTT 2160

TGTAAAAAAT TTCTATATAA AATATTGAA ACTTAA 2196

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(2) INFORMATION FOR SEQ ID NO: 283:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1185 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

GCAGTTAAGG CTTCTGATAA GGAAAGAGAG TCTGAACAGA GCACACACAT CTGGAGCTCC 60

20 AGGAGTGGGG GATGCAGCAT CAGATTCCAT CTTGAATTTC TGCTAAAATA CTTTGTACTC 120

ATAATGGATC TCAACAAAGA TCTGTATTTC ATCTGTGGCT CCATCTTCCC TCTGGGTCAA 180

25 GTAGATGTTA AGCTGGACCT TGGCACGCCT CTTAACATGA AGAGATCTAG CTAGACAGAC 240

AGACTCCCCC ATTTATGGGA ACAAGAATTC AATTTATTCT CTATTTATAA AACATTTTTT 300

TAAAGTGCCT TGGGTATAAA AATCTAAATG TCTGCGGTGT GATCAGTCAG GAGCACGTAA 360

30 CTATCACTCT TCGCATCCTT TGGTCACTGG GAGATCCTTT GGGGGCTGGG AGGTCCTTCT 420

GTCCAGGCT AAAGGAAAAG CTTACAAGG GTAAGAGCCA CAGAACCCTC GGCAAGAAAG 480

35 GCCGGTCAGG GAGAATGAAT GGTACAGAGA GGAAAGGAAG GAAAGGGGGT GGAACAGAGG 540

TAGAAGGCAA GGAAGGGATG CCGCACTGGA GACCGATGGG GACACTCTAA TTGTGCAAGA 600

GGGAGGATCT TCCTTCTTGA ATGCTGAACA CAGCTAGTCT GAACCTTCCT TGGAAAGTCC 660

40 AGCTGTTTGC CCATGCATAG GGCCAACTCT CCCTGCAAAG CAGCAAATGT GGCTTCTATC 720

AGGAAGGAAA AGTATCCATC AGTGTGACAA GAGGTCACCT TCGAACTTGC ATGAACCTCT 780

45 TGCGCAGCCA CAAAGAGTCC TGGTAGAAGT GAGGATCGCC TAGTCTTACG GCTGTCCGTT 840

TATAGAAGTA GCAGTACAAC ACTGCTGCTA GTCTCTGGAA TACAAACAGC ATTTGAAGTC 900

CATCTGTCCA TATGAAGCTG TTGGAGTTTT TCCAGCGTAA GTTCATGACC CAGACATGAA 960

50 GGGAGATGCT GAGGGCAAAG TACACAGCTG TCAGGATGAT GGTCCCTTTG AACTTATGGA 1020

ATAGGAGGTT GACCAGGCCA GCCTGGAAGA CGAAGGTGTT GAAGAACATG AGGAAAATGA 1080

55 TGATGATGTT GAAGAGGACT GCAATATCCT GGATGCACTG AGGGAGAGGY TTCTAGTTCC 1140

TTTGAATGAG AGCTGTTTCC CTTGCTCTAA GGCAAGCACC TCCAA 1185

60

## (2) INFORMATION FOR SEQ ID NO: 284:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

10

AGGGAAAGGG GAGGGTAGCG GGAGGGTAGC AGGTGAGTTC CTAGGGCTGG AAGGTTTAGC 60  
AGCAGCCTGG TGCAGTGCCC TGTATCAAG ACAAAACCCAC GGTCTCTMCTG GGTGCCTACC 120  
15 AAGCTTGGTT TGTACAAAAG CAAGGTGGGA GTCTATTTT GTACATGAGA TACATCACAC 180  
TTACCTGTGG GCCAGTATTG TGAAGTGAGT CTGAGTTGTT TACACTGATG CCTTCCCTGC 240  
CCACCACAAA TTGTGTACAT AGTCTTCAGA TGATACCACC CCTTTCCCA GCTCCCAACC 300  
20 AAGAGCTGGT TCTAGGCCTG TGTATATGT CATATTTAGC STTTTATAT ATGACCTTGG 360  
ATTCTGTGTG TTTGTATTT AGCACAGTGT ATGCACCTTC ATTTAAATAC ATCTGTGTGC 420  
25 ATACAGATAC GCATATATGT GTGTGCGTAT GCATATATCT CTCATCTGTA GTTCCAAGA 480  
GTTCACTGA AGCAGATGGA GTCTGCAGC CCAGGAGACA CCTGCATCC CTGCTAATAG 540  
TGTTTGCCAC AAGTATTAGT GAGTCTTCCT TATTAATATT TTCATTTTCAAG AAGACTGAAG 600  
30 CAAAGCTGAT AGTGTTTGCT GTTCTTTGG CAGCTAAGTG AGGGTCTTGG GATGACTTGC 660  
TGTTTCCTC AAGCTGCACT TTGGGGCCAT CTCTGCAGTA TTAGCCCCCT TTTTGCTTGG 720  
35 TGTACTCTG TCTGTGCCG TGTGTGTGTG TGATAGTCAC TCTTGCATGG CTTCATGTC 780  
TGGTTTGTGG CATTGGGGA TAAGTGCTG AAGCCAGAGC ATTTGCAGTT TGTTGAGGC 840  
CTCGTTGCCA ATGATAGATC ACTCTGTGTG ACCTGGTATG TCTGCTTGCT TGCTGCTTTT 900  
40 CCTGCTTTC TCTTGAAGA GGAAAGGACT CTGGTCAGGC CCAGGCTGAG TGAGATGAGC 960  
TGCAGCTGGC TCATGGCCTT CTTAGAGCAG AGAGAGGAGT ATGTCATTTT ACTAAGTTCC 1020  
45 TAAACAAACA TTTATGCAGG CAACACTCCT TGCAGATCCA GAAACTGAGG CACAATAGGG 1080  
TTATGACTTG CTCAAGAATA TGTAGCTGCT AGGGGGTAAA TCAAGGCATC ACAATTCTG 1140  
TTCAGCGGGC AGGAATAGGC TGTGAATTGC TAGCACTTTT TTTTTTAAG CAATTACTTT 1200  
50 TTGACTTGTT CCTCTGAAAG TGCAAGAGGC GTACACCTTT CCCAAATGTA GACTAGAATC 1260  
TGCAGGATGC CACCCACTGT ATAGTTCTGC TTTCCCAGAG AGGAAGAACT TTTAGAAACC 1320  
55 AAATGATCTT AATTGTTATT GCCCACCCCT GGCTTTTCCG GGTAGAAAAT TCACAGTAGG 1380  
AATGATTGTT AAGAGAGAGT GCTTGAACC ATGGGTTAAC AGGAAAGGCT ACCTAACTTC 1440  
ACATATCTGC AACCAGAGCA GCCACCAAGC ATTACTTAGC AGCAGGAAAA TGATTGTATT 1500  
60

TGAGTTCTCG TGTGTCCAAA ACTGAGGCAC CATGTTCTTT GAAAACATGC CACCTCAAGG 1560  
 CTGGGCGCGG TGGCTCACAC CTGTAATCCC AGCAYTTTGG GGAGGCCSAG GCGGGGCGG 1620  
 5 KTTCAACCGG GGTG 1634

10 (2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1795 base pairs  
 (B) TYPE: nucleic acid  
 15 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

20 TTCCCCCAG GTTGCTTCC TTCGATTCCT TTTCTTGGTA TCAACGTTTG ATTGAAGAA 60  
 CAACCCCTC TTTGTCAACC TCAATAATGA GCTCACTGTG GAGGAGCAGC TCGGGCACAG 120  
 25 CTCMCCGTYA TGGTCATTGT TACCCCCCAA GACCGCAAAA ACTCTGTGTG GACACAGGAT 180  
 GGACCCTCAG CCCAGATCCT GCAGCAGCTT GTGGTCCTGG CAGCTGAAGC CCTGCCCATG 240  
 TTAGAGAAGC AGCTCATGGA TCCCCGGGGA CCTGGGGACA TCAGGACAGT GTTCCGGCCG 300  
 30 CCCTTGGA CA TTTACGACGT GCTGATTCGC CTGTYTCTTC GCCATATCCC GCGGCACGCG 360  
 AGGCTTGTTG ACTGCCAGY TGCCTCCTTC TGCCGGGGCC TGCTCAGCCA GCCGGGGCCC 420  
 TCATCCCTGA TGCCCGTGCT GGGTATGAT CCTNCTCAGC TCTATCTGAC GCAGCTCAGG 480  
 35 GAGGCCPTTG GGGATCTGGC CCTTTCTCTC TATGACCAGC ATGGTGAGA GGTGATTGGT 540  
 GTCTCTGGA AGCCACCAG CTTCACGCG CAGCCCTTCA AGGCCTCCAG CACAAAGGG 600  
 40 CGCATGGTGA TGTCTCGAGG TGGGAGCTA GTAATGGTGC CCAATGTTGA AGCAATCCTG 660  
 GAGGACTTGT CTGTCTGGG TGAAGGCTG GTGCAGACTG TGGAGCCCCG AAGTGAGAGG 720  
 TGGACTGTGT GATCCAGCT CTGGAGCAAG CTGTAGACGG ACAGCAGGAC ATTGGACCTC 780  
 45 TAGAGCAAGA TGTCAGTAGG ATGACCTCCA CCTTCTTGG ACATGAATCC TCCATGGAGG 840  
 GCCTGCTGGC TGAACATGCT GAATCATCTC CAACAAAACC CAGCCCCAAC TTTCTCTCTG 900  
 50 ATGCTCCAGC ATTGGGGCAG GGGCATGGTG GCCCATGTAG TCTCCTGGGC CTCACCATCC 960  
 CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA GGAAGTGAAC CCAGGAGATC CATCCACCTA 1020  
 TTAGCCCTGG CCCTGGACCT CCTGCGATT TCCCACTCCT TTCTTAGTCT TCTTCCAGAA 1080  
 55 ACAGAGAAGG GGATGTGTG CTGGGAGAGG CTCTGTCTCC TTCTGCTGC CAGGACCTGT 1140  
 GCCTAGACTT AGCATGCCCT TCACTGCAGT GTCAGGCCTT TAGATGGGAC CCAGCGAAAA 1200  
 60 TGTGGCCCTT CTGAGTCACA TCACCGACAC TGAGCAGTGG AAAGGGGCTA TATGTGTATG 1260

AATAGACCAC ATTGAAGGAG CACAATGCCC TCCTGTGTTG ATGCCACTTC CCAGGGTGGG 1320  
 5 GACAGTGGAA AAGAACCGAG GACAGGAAAG GATTGGGTAG GTGAAGGGGT CAGGGGACTG 1380  
 GTAGTACCCC AATCTTGGAG AGGTGCAAAA AGCACTGGGG GCTACCCGTT AGCTGCATCT 1440  
 GCCCTGGCTG TTTGCCCGTT CATGTCACAA ACTGCCACTA CTATGTACCT GCAGTGGGGT 1500  
 10 TGCAGAGATG GGGGAGACTC AAGTCTTACT CCCCAGGAGC TCCCAGGGCC CAAGGAGGAG 1560  
 AATGCTGCCT CCTTTCAGTC TGGTCTACAC CCACTTTCCTG GTAGCCTCTC TGCTTCCTGT 1620  
 AATCTGGGT GTTTTCCAG ACTCAGCTCA AATAGTCCC CTCTTAAGC CCATCCCTCG 1680  
 15 CCCCAGCCT GAGGTGATCT TTCCCTCTC TGAATAITA GAGCAGTTAC TGTCGTTC 1740  
 GTTCGTTGG CAGGCACACA CAGTGGCATA AATCTATTG TTTTGAACTC TGATT 1795

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(2) INFORMATION FOR SEQ ID NO: 286:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 858 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCTGCTTTCG GTGCTGCGTG TACTGCTGGG CGGCTTCTTC GCGCTCGTGG GGTGGCCAA 60  
 35 GCTCTCGGAG GAGATCTCGG CTCCAGTTTC GGAGCGGATG AATGCCCTGT TCGTGCAGTT 120  
 TGCTGAGGTG TTCCCGCTGA AGGTATTTGG CTACCAGCCA GATCCCTGA ACTACCAAT 180  
 40 AGCTGTGGGC TTTCTGGAAC TGCTGGCTGG GTTGCTGCTG GTCATGGGCC CACCGATGCT 240  
 GCAAGAGATC AGTAACTTGT TCTTGATTCT GCTCATGATG GGGGCTATCT TCACCTTGGC 300  
 AGCTCTGAAA GAGTCACTAA GCACCTGTAT CCCAGCCATT GTCTGCCTGG GGTTCCTGCT 360  
 45 GCTGCTGAAT GTCGCCAGC TCTTAGCCCA GACTAAGAAG GTGGTCAGAC CCACTAGGAA 420  
 GAAGACTCTA AGTACATTCA AGGAATCCTG GAAGTAGAGC ATCTCTGTCT CTTTATGCCA 480  
 TGCAGCTGTC ACAGCAGGAA CATGGTAGAA CACAGAGTCT ATCATCTTGT TACCAGTATA 540  
 50 ATATCCAGGG TCAGCCAGTG TTGAAAGAGA CATTTTGTCT ACCTGGCACT GCTTTCCTT 600  
 TTTAGCTTTA CTACTCTTTT GTGAGGAGTA CATGTTATGC ATATTAACAT TCCTCATGTC 660  
 55 ATATGAAAT ACAAAATAAG CAGAAAAGAA ATTTAAATCA ACCAAAATTC TGATGCCCCA 720  
 AATAACCACT TTTAATGCCT TGGTGTAAGT ATACCTCTGA ACTTTTCT GTGCCTTTAA 780  
 60 ACAGATATAT ATTTTTTTT AATGAAAATA AAACCATATA TCCTATTTTA TTTCTCCTT 840

TTAAACCTT ATAACTA

858

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(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 915 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

15

GAATTCGGCA CGAGCGGGC CATGGCGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC 60

GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCTCGGAGG AGATCTCGGC TCCAGTTTCG 120

20

GAGCGGATGA ATGCCCTGTT CGTGCACTTT GCTGAGGTGT TCCCGCTGAA GGTATTTGGC 180

TACCAGCCAG ATCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAAGT GCTGGCTGGG 240

25

TTGCTGCTGG TCATGGGCCC ACCGATGCTG CAAGAGATCA GTAACTTGTT CTTGATTCTG 300

CTCATGATGG GGGCTATCTT CACCTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360

CCAGCCATTG TCTGCCTGGG GTTCCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCCAG 420

30

ACTAAGAAGG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480

AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540

35

ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGGT CAGCCAGTGT TGAAAGAGAC 600

ATTTTGTCTA CCTGGCACTG CTTTCTCTTT TTAGCTTTAC TACTCTTTTG TGAGGAGTAC 660

ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720

40

TTTAAATCAA CCAAAATTCT GATGCCCCAA ATAACCACTT TTAATGCCTT GGTGTAAGTA 780

TACCTCTGAA CTTTTTTCTG TGCCTTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840

45

AACCATATAT CCTATTTTAT TTCCTCCTTT TAAACCTTA TAAACTATAA MAAAAAAAAA 900

AAAAAAAAAA CTCGA 915

50

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 1517 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

60

	CCTTGTTGGCA ACTAGTGGGT CCCCGGGCT GCAGNAATTC GGGCAGTGGT TCTGNGTCTG	60
	AAGATACTCT GAGTTCTCTCT GAGAGATCCA AAGGCTCCGG GAGCAGACCC CCAACCCCCA	120
5	AAAGCAGCCC TCAGAAGACC AGGAAGAGCC CTCAGGTGAC CAGGGGTAGC CCTCAGAAGA	180
	CCAGCTGTAG COCTCAGAAG ACCAGGCAGA GCCCTCAGAC GCTGAAGCGG AGCCGAGTGA	240
10	CCACCTCACT TGAAGCTTTG CCCACAGGAC AGTGCTGACA GACAAGAGTG GGCGACAGTG	300
	GAAGCTGAAG TCCTTCCAGA CCAGGGACAA CCAGGGCATT CTCTATGAAG CTGCACCCAC	360
	CTCCACCCCTC ACCTGTGACT CAGGACCACA GAAGCAAAAG TTCTCACTCA AACTGGATGC	420
15	CAAGGATGGG CGCTTGTTC A TGAGCAGAA CTCTTCCAG CGGGCCGCCA AGCCTCTGCA	480
	AGTCAACAAG TGGAAGAAGC TGTACTCGAC CCCACTGCTG GCCATCCCTA CCTGCATGGG	540
20	TTTCGGTGT T CACCAGGACA AATACAGGTT CTGGGTGTTA CCCAGCCTGG GGAGGAGCCT	600
	TCAGTCGGCC CTGGATGTCA GCCCAAAGCA TGTGCTGTGC AGAGAGGTCT GTGCTGCAGG	660
	TGGCCTGCCG GCTGCTGGAT GCCCTGGAGT TCCTCCATGA GAATGAGTAT GTTCATGGAA	720
25	ATGTGACAGC TGAAAATATC TTTGTGGATC CAGAGGACCA GAGTCAGGTG ACTTTGGCAG	780
	GCTATGGCTT CGCMTCCGC TATTGCCCAA GTGGCAAACA CGTGGCCTAC GTGGAAGGCA	840
30	GCAGGAGCCY TCACGAGGGG GACCTTGAGT TTCAATTAGCA TGGACCTGCA CAAGGGATGC	900
	GGGCCCTCCC GCCGCRGYGA CCTCCAGAGC CTGGGYTAMT GCATGCTGAA GTGGYTCTAM	960
	GGGTTTCTGC CATGGACAAA TTGCCTTCCA AMAMTGAGGA CATCATGAAG CAAAAACAGA	1020
35	AGTTGCCTTG GGATTCATTT TAATGTAAGC TKGACTTTGT CATGCCAGAA ACAAGGCTCG	1080
	GTCACCGTCA GCAGTTTGCA GTTTTCCACC TCCWCCAGT TCCTCCGTGT GGTTGACCCA	1140
40	GATATCTCCG TTATGCAGCC GCCTCCGGGG GACCACCTCC CTCCCTTTGA GTCAGCCACA	1200
	GACAGCCTAC TTGACGGCCC CGCTGGCCCC CACATTCAC TGAAGTGTGC GGATGCCACA	1260
	GTGACCCCTC CTCAGGCACA GCATGACCTC CTGAAGTCGA GCCTGCTTGC TTTGAACCTA	1320
45	CCAGTAAAAA TCTCTCAAA ATGTTTGAT ACCGCCCAT GGGCCCTCAC AGCCACGAGC	1380
	TCCCTGACCA GTGTGCGTGT GTGTGTGTGT GTGTGTCTGT GTGTGTGCTT GGGACGGGTG	1440
50	GGGAGGTAC CTTTGGGTGT GCGGTGTGCC CCCAGGACCT GTAAGTAATA AAATCTTTAT	1500
	TTCCAAAAAA AAAAAA	1517

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(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3865 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

5	TGGAGGGGGG GAGCTTCCTT GAGCAGTGGG CCCAGGCCTG GCCCTCCACA CTTCATTCTC	60
	TGACCTTTCT CTCTCCTCAT TTCGGTGCAT GTCCTTTCCTG CAGCTGCCTT TCAGCACAGG	120
10	TGGTTCCACT GGGGGCAGCT AACGCTGAGT GACAAGGATG GGAAGCCACA GGTGCATTTT	180
	ACTCAAGTCT TCTCTAGTCA ATGAGGGGCA CCCAGTGCTT CTAGGGCAGG CTGGGTGGTG	240
	GTCCCTTAGG TATCAGCCTC TCTTACTGTA CTCTCCGGGA ATGTTAACCT TTCTATTTTC	300
15	AGCCTGTGCC ACCTGTCTAG GCAAGCTGGC TTCCCCATTG GCCCTGTGG GTCCACAGCA	360
	GCGTGGCTSC CCCCCAGGGC CACCGCTTCT TTCTTGATCC TCTTTCCTTA ACAGTGACTT	420
20	GGGCTTGAGT CTGGCAAGGA ACCTTGCTTT TAGCTTCACC ACCAAGGAGA GAGGTTGACA	480
	TGACCTCCC CCCCCCTCAC CAAGGCTGGG AACAGAGGGG ATGTGGTGAG AGCCAGGTTC	540
	CTCTGGCCCT CTCCAGGGTG TTTTCCAATA GTCACACTG TCTTCTCCTT GTAGCTAATC	600
25	AATCAATATT CTTCCTTGC CTGTGGGCAG TNGGAGAGTG CTGCTGGGTG TACGCTGCAC	660
	CTGCCCACTG AGTTGGGGAA AGAGGATAAT CAGTGAGCAC TGTCTGCTC AGAGCTCCTG	720
30	ATCTACCCCA CCCCCTAGGA TCCAGGACTG GGTCAAAGCT GCATGAAACC AGGCCCTGGC	780
	AGCAACCCTG GGAATGGCTG GAGGTGGGAG AGAACCTGAC TTCTCTTTCC CTCTCCCTCC	840
	TCCAACATTA CTGGAATCT ATCCTGTTAG GATCTTCTGA GCTTGTTTCC CTGCTGGGTG	900
35	GGACAGAGGA CAAAGGAGAA GGGAGGGTCT AGAAGAGGCA GCCCTTCTTT GTCTCTGGG	960
	GTAAATGAGC TTGACCTAGA GTAAATGGAG AGACCAAAG CCTCTGATTT TTAATTTCCA	1020
40	TAAAATGTTA GAAGTATATA TATACATATA TATATTCTT TAAATTTTGT AGTCTTTGAT	1080
	ATGTCTAAAA ATCCATTCCC TCTGCCCTGA AGCCTGAGTG AGACACATGA AGAAAAGTGT	1140
	GTTTCATTTA AAGATGTTAA TTAAATGATT GAAACTTGGC TGTGGCTACT GCTTCTTAAT	1200
45	GTTGGGGGA CAGGGCAGTG GTCTGGGCC ACATTTAGAA GGGAAAATGT TTTGCCTGCT	1260
	GCACACATTG GACCCAAGTA TGGGCTCTT CTGCCTAGTA CTGCCAAAG GACTGTTAAG	1320
50	GTGTCTTGTC CATCTTCTAC CCCCCACCC CCATTACGGG TAAAGGRAAC CCCAGACTAG	1380
	GTGAGGGGCC AGCAGCTGCC TCACATTGTG TTCTCTCTG AGATGGTCCA GCTCACATCC	1440
	AGACACCTTG TTCAGACATT TTATTTGAAT TTATGACAGT GATGGGGATT TGACTGAGAT	1500
55	GCCTTATGGA GAAGTACCCC ACCCTCTATG AAGACAGAAT CACTCTCTGC CATTCATTCT	1560
	GCCTGATGCT AACAACACGC AGCTGATTTA GGGAGTGTCC CAGCCTAGCT GGATCAAGGG	1620
60	AAATTCCAGG AGCCCTGGGG CAGGCCCTGG NCCCCAGTGC CAAGCCTCAG AGTAAGCAGA	1680

	CATTGGGAAA GTTGCCAACC ACTTGGTAGA CCACTAGGTT CTCTGTTTTT CCTTCCCTTT	1740
5	CCTTTTCAAA TCCACAGTT TCCTGTTGGG GAGAAGCTGT AATTAGCCTA GTCCAGGTAC	1800
	CAGATCCCAG CTAGGGGGC AGCTGNCITG GATAACTCCA AGAAAACCTG GGCACCAGTA	1860
	TTTTTCCAAT TATAAGGACT GTGGCATAAA TTTTAAATG AGTTATATTG AAACCAGATT	1920
10	TCTCCAGCTG CCAAGGGAAG AAGGTAGGGC TGGACTCCCT GCTGTGGCCC AGCCCTTGT	1980
	AGGGGTGGT CTCTACTGC AGCCAGACAG GATGATCCTG GGTTCGGGG AGGGTAAGCT	2040
15	GCCCCTTGCC GAGTTCGCA CCGAATAAAG AGTCCAAACC CGCTGCTTCC GTGTCTGAG	2100
	AGATGGGTAA ATGGGTGATG GATGGAGCAG ACTGAAGAGA CAGCAGATGA CTCAGTGGTG	2160
	GAAGAAGGGG GGAAGATGCT GGGCTGGCTA GCTAATGTTT CCCCTTTTCA GCGATTTACA	2220
20	GGAAATGGAG CCCAGCTTGG TCATGAAGTT GGTTCGCTTC CACTGTGCGA TGCACTCCTC	2280
	AGAAATTTTG AAGTCAGCCT GCAACTTCTC GAAGACTTTC TTCTTGGGCT TGAGCTCCTC	2340
25	ATCTGGTTGG CCCTTTTCAT AGCCCTTCAC AAACACGTGC TCACCAGGAG CAGAGCCTGC	2400
	CGGAGGTGCC AGAGGTTCAA CTGGCGGTTT ATCCCTTCTA TAGAAGCACA CAGAAGCATG	2460
	CCTTGGGACT CGACTCCTCT CATCTTCTGG GGTTCAGGT TGCACAGCAC CACTACCAGC	2520
30	CTGTCTGCA GTTCTCCTT GGGCAGCAAC TGTACCAGGC CGCTCACCAC AGTCCGTGGT	2580
	TCAGCTTCCC CCACGTCAAT CTTCTCTACA TACAGGCTGT CTGCATCTGG GTGCTTCTCC	2640
35	ACAGTGATGA TTTTCCCCAC ACGGATATCC AGCCGGGATG GGATGACCTC CTCTGGTTCT	2700
	GAATCTTGG CAGGCCCTTG GCCATTGGCT TCTGCTTTGA GGGATCTGGG TAGGCAGCGC	2760
	TGGCCAGTTT TTTCAGGGCA GGGGTATTAA ACTTTTCCCG GATTGGATCC AGCAACTTGT	2820
40	TCAGTGGAC TTCAACAGAA TTCTTCAGGT CTCCAGGATG TACAACCTCA GCAGCAAAGT	2880
	CCTTTTCCAG GTCCACGTAA GCTGTGTAGG TTTTGTTC ACCCCATTTC TCATCTCGTA	2940
45	GGATCAGAAA CTCGGACTTA AGGGGAAAAA GGACATGCTT GATGAAGGAC AGAACCCCAT	3000
	TGTTCTCCAC ATTTCTGGC TCACAGAAGG CCTTCTTCAG TTTTTCCTTC ACATCCTCCT	3060
	TCCGATCAAG GAGATCAATC TTGGACTCCT CTCTGAAGA GCTCATTTTG CTGCCCTGTA	3120
50	ATCCTGGAAC CATAGGATTC ATCAGATGGA CCGTTTTGA ATAGCCAAGT GCAGGGAGGT	3180
	ACTTCTCTGC AAAGGTGAAA ATCTTCTCT GATCAATGCC TCCAAATTGG GCATCTACTT	3240
55	TTAAATACTC TTCATCCAAA GCCTGCAGTC CGGGGTATAA GAGGCCACTC AGCAAAGGGT	3300
	GCTCCACCTG CTTTACCACC TCAGCTCCAG CCTTCTTGA ATCGTGTCTGT GTGACCACGG	3360
	AGGAGAGTCT GTACACATCT AGTGTGTACT CTTTGTCTGAG CTGGTAATCA GTGCCTTTGA	3420
60	TGAACTTGAG CTCTCCAAG GGCACACCAA TGCTCTCCAG CATTCCTTTG ATCACATTCT	3480



CATAGTAACT GACTCGGAGT TCTAGAAGTT CCCATGGGGC TTTCATGTTA TCCAGGTATG 3540  
 CGTGGAGGTC CGCAAACAGA ATTGTTACCT CACACCCCTGC CTTTAAGAAG TCTGCAATCT 3600  
 5 TTGACATGGG CACAAAAGTAA GCCACATGTG GTTTGCCCGT GGTTCGCGTT CCCCAGTAAA 3660  
 TTTTAAGTTC CCGTCCTTC AGTATCTCCT TCAGCTTCTC TTCCCCCAGA ACCTCCTGCA 3720  
 10 GGTTCGCGGT GATAAGGTGC AGTTTCTCTT CAGGGCTGGG AGCGTCCCC ATGGTCCGCT 3780  
 ACCCCTGCTT CCCCCTCA GCCCGGCACC AGAGCCCTT CCTGGGTAC CGTCGCGGC 3840  
 15 GCGTCCCGG AACTGTCACG CGAGT 3865

## (2) INFORMATION FOR SEQ ID NO: 290:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1910 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

AGGGAGAGGA GGAGAGGGG TCTGCGCGG GCCCTACCC AGAAGCCAGC GGACGGCAGC 60  
 30 ACGGAGTGGG CTGTCCCCGA GCCCAGCCCC GAGCGAGCCC CCCCCCGGC CCCGMAGGAC 120  
 GCGCTYCCA GCCAGCCCA CTCCTAGGAG GAGGGAGGC GGGAAAGCAG CTCAGCCTC 180  
 35 ACCCACCGCC CTGCCCCCAG CCCCCTCACT CCCAGGCTCC TCGGACTCG GCGGGTCTC 240  
 CTGGAGTCT CGGAGGGGAC CGNCTGTGCA GACCCATGG AGTTGGTGCT GTCTTCCTC 300  
 TGCAGCCTGC TGGCCCCCAT GTCTCTGCC AGTGCAGCTG AAAAGGAGAA GGAAATGGAC 360  
 40 CCTTTTCATT ATGATTACCA GACCTGAGG ATTGGGGGAC TGGTGTTCG TGTGGTCTC 420  
 TTCTCGGTTG GGATCTCCT TATCCTAAGT CGCAGGTGCA AGTGCAGTTT CAATCAGAAG 480  
 45 CCCCAGGCC CAGGAGATGA GGAAGCCAG GTGAGAACC TCATCACCG CAATGCAACA 540  
 GAGCCCCAGA AAGCAGAGAA CTGAAGTGCA GCCATCAGGT GGAAGCCTCT GGAACCTGAG 600  
 GCGGCTGCTT GAACCTTTGG ATGCAAATGT CGATGCTTAA GAAAACCGGC CACTTCAGCA 660  
 50 ACAGCCCTTT CCCCAGGAGA AGCCAAGAAC TTGTGTGTC CCCACCTAT CCCCTCTAAC 720  
 ACCATTCTC CACCTGATGA TGCAACTAAC ACTTGCCTCC CCACTGCAGC CTGCGGTCT 780  
 55 GCCACCTCC CGTGATGTGT GTGTGTGTGT GTGTGTGTGT GACTGTGTGT GTTTGCTAAC 840  
 TGTGGTCTTT GTGGCTACTT GTTTGTGGAT GGTATTGTGT TTGTTAGTGA ACTGTGGACT 900  
 CGCTTTCCCA GGCAGGGGCT GAGCCACATG GCCATCTGCT CCTCCCTGCC CCGTGGGCC 960  
 60

	TCCATCACCT TCTGCTCTA GGAGGCTGCT TGTGCCCCGA GACCAGCCCC CTCCCCTGAT	1020
	TTAGGGATGC GTAGGGTAAG AGCACGGGCA GTGGTCTTCA GTCGTCTTGG GACCTGGGAA	1080
5	GGTTTGACAG ACTTTGTCAT CATCTTTCAT GGACTCCTTT CACTCCTTTA ACAAAAACCT	1140
	TGCTTCCTTA TCCCACCTGA TCCAGTCTG AAGGTCTCTT AGCAACTGGA GATACAAAGC	1200
	AAGGAGCTGG TGAGCCCAGC GTTGACGTCA GGCAGGCTAT GCCCTTCCGT GGTTAATTTC	1260
10	TTCCCAGGGG CTTCACGAG GAGTCCCCAT CTGCCCCGCC CCTTCACAGA GCGCCCGGGG	1320
	ATTCCAGGCC CAGGGCTTCT ACTCTGCCCC TGGGAATGT GTCCCCTGCA TATCTTCTCA	1380
15	GCAATAACTC CATGGGCTCT GGGACCCCTAC CCCTTCCAAC CTTCCTGCT TCTGAGACTT	1440
	CAATCTACAG CCCAGCTCAT CCAGATGCAG ACTACAGTCC CTGCAATGG GTCTCTGGCA	1500
	GGCAATAGTT GAAGGACTCC TGTTCGGTGG GGGCCAGCAC ACCGGGATGG ATGGAGGGAG	1560
20	AGCAGAGGCC TTTGCTTCTC TGCTTACGTC CCCTTAGATG GGCAGCAGAG GCAACTCCCG	1620
	CATCCTTTGC TCTGCCGTGC GGTGGTCAGA GCGGTGAGCG AGGTGGGTG GAGACTCAGC	1680
25	AGGCTCCGTG CAGCCCTTGG GAACAGTGAG AGGTGAAGG TCATAACGAG AGTGGGAAT	1740
	CAACCCAGAT CCGCCCTCT CTGTCTCTG TGTTCCTCGG GAAACCAACC AAACCGTGG	1800
	CTGTGACCCA TTGCTGTCT CTGTATCGTG ATCTATCCTC AACACAACA GAAAAAGGA	1860
30	ATAAATATC CTTTGTTCM TAAAAA AAAAAGGGGGG	1910

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(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 3276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

	GCGACCGTCG TTTGAGTCGT CGCTGCCGCT GCCGCTGCCA CTGCCACTGC CACCTCGCGG	60
	ATCAGGAGCC AGCGTTGTTT GCCCGACGCC TCGCTGCCG TGGGAGGAAG CGAGAGGGAA	120
50	GCCGCTTGCG GGTGTGTCG CGCTGCTCG CCACCGCTG GAAGAGCCGA GCCCGGCCCC	180
	AGTCGGTCGC TTGCCACCGC TCGTAGCCGT TACCCGCGGG CCGCCACAGC CGCCGGCCGG	240
	GAGAGGCGCG CGCCATGGCT TCTGGAGCCG ATTCAAAAGG TGATGACCTA TCAACAGCCA	300
55	TTCTCAAACA GAAGAACCGT CCCAATCGGT TAATTGTTGA TGAAGCCATC AATGAGGACA	360
	ACAGTGTGGT GTCCTGTGCC CAGCCCAAGA TGGATGAATT GCAGTTGTTT CGAGGTGACA	420
60	CAGTGTGCT GAAAGGAAAG AAGAGACGAG AAGCTGTTT CATCGTCCTT TCTGATGATA	480

	CTTGTTCGTA TGAGAAGATT CGGATGAATA GAGTTGTTTCG GAATAACCTT CGTGTACGCC	540
5	TAGGGGATGT CATCAGCATC CAGCCATGCC CTGATGTGAA GTACGGCAAA CGTATCCATG	600
	TGCTGCCCAT TGATGACACA GTGGAAGGCA TTAGTGGTAA TCTCTTCGAG GTATACCTTA	660
	AGCCGTAATT CCTGGAAGCG TATCGACCCA TCCGGAAGG AGACATTTTT CTTGTCCGTG	720
10	GTGGGATGCG TGCTGTGGAG TTCAAAGTGG TGGAAACAGA TCCTAGCCCT TATTGCATTG	780
	TTGCTCCAGA CACAGTGATC CACTGCGAAG GGGAGCCTAT CAAACGAGAG GATGAGGAAG	840
15	AGTCCTTGAA TGAAGTAGGG TATGATGACA TTGGTGGCTG CAGGAAGCAG CTAGCTCAGA	900
	TAAAGGAGAT GGTGGAACGT CCCCTGAGAC ATCCTGCCCT CTTTAAGGCA ATTGGTGTGA	960
	AGCCTCCTAG AGGAATCCTG CTTTACGGAC CTCTGGAAC AGGAAAGACC CTGATTGCTC	1020
20	GAGCTGTAGC AAATGAGACT GGAGCCTTCT TCTTCTTGAT CAATGGTCCT GAGATCATGA	1080
	GCAAATGGC TGGTGAGTCT GAGAGCAACC TTCGTAAAGC CTTTGAGGAG GCTGAGAAGA	1140
25	ATGCTCCTGC CATCATCTTC ATTGATGAGC TAGATGCCAT CGCTCCCAA AGAGAGAAAA	1200
	CTCATGGCGA GGTGGAGCGG CGCATGTAT CACAGTGTGT GACCCCTCATG GATGGCCTAA	1260
	AGCAGAGGGC ACATGTGATT GTTATGGCAG CAACCAACAG ACCCAACAGC ATTGACCCAG	1320
30	CTCTACGGCG ATTTGGTCCG TTGACAGGG AGGTAGATAT TGGAAATTCCT GATGCTACAG	1380
	GAGCTTAGA GATTCTTCAG ATCCATACCA AGAACATGAA GCTGGCAGAT GATGTGGACC	1440
35	TGGAACAGTA GCCAATGAGA CTCACGGGCA TGTGGGTGCT GACTTAGCAG CCCTGTGCTC	1500
	AGAGGCTGCT CTGCAAGCCA TCCGCAAGAA GATGGATCTC ATTGACCTAG AGGATGAGAC	1560
	CATTGATGCC GAGGTATGA ACTCTTAGC AGTTACTATG GATGACTTCC GGTGGGCCTT	1620
40	GAGCCAGAGT AACCCATCAG CACTGCGGGA AACCGTGGTA GAGGTGCCAC AGGTAACCTG	1680
	GGAAGACATC GGGGGCTAG AGGATGTCAA ACGTGAGCTA CAGGAGCTGG TCCAGTATCC	1740
45	TGTGGAGCAC CCAGACAAAT TCCTGAAGTT TGGCATGACA CCTTCCAAGG GAGTCTGTGT	1800
	CTATGGACCT CCTGGCTGTG GGAAACTTT GTTGCCAAA GCCATTGCTA ATGAATGCCA	1860
	GGCCAACCTC ATCTCCATCA AGGGTCCTGA GCTGCTCACC ATGTGGTTTG GGGAGTCTGA	1920
50	GGCCAATGTC AGAGAAATCT TTGACAAGGC CCGCAAGCT GCCCCTGTG TGCTATTCTT	1980
	TGATGAGCTG GATTGATTG CCAAGGCTCG TGGAGTAAC ATTGGAGATG GTGGTGGGGC	2040
55	TGCTGACCGA GTCATCAACC AGATCCTGAC AGAAATGGAT GGCATGTCCA CAAAAA	2100
	TGTGTTATC ATTGGCGCTA CCAACCGGCC TGACATCATT GATCCTGCCA TCCTCAGACC	2160
	TGGCCGTCTT GATCAGCTCA TCTACATCCC ACTTCTGAT GAGAAGTCCC GTGTTGCCAT	2220
60	CCTCAAGGCT AACCTGCGCA AGTCCCCAGT TGCCAAGGAT GTGGACTTGG AGTTCCTGGC	2280

	TAAAATGACT AATGGCTTCT CTGGAGCTGA CCTGACAGAG ATTTGCCAGC GTGCTTGCAA	2340
	GCTGGCCATC CGTGAATCCA TCGAGAGTGA GATTAGGCGA GAACGAGAGA GGCAGACAAA	2400
5	CCCATCAGCC ATGGAGGTAG AAGAGGATGA TCCAGTGCCT GAGATCCGTC GAGATCACTT	2460
	TGAAGAAGCC ATGCGCTTTG CGCGCCGTTT TGTCAGTGAC AATGACATTC GGAAGTATGA	2520
10	GATGTTTGCC CAGACCCCTTC AGCAGAGTCG GGGCTTTGGC AGCTTCAGAT TCCCTTCAGG	2580
	GAACCAGGGT GGAGCTGGCC CCAGTCAGGG CAGTGGAGGC GGCACAGGTG GCAGTGTATA	2640
	CACAGAAGAC AATGATGATG ACCTGTATGG CTAAGTGGTG GTGGCCAGCG TGCAGTGAGC	2700
15	TGGCCTGCCT GGACCTTGTT CCCTGGGGGT GGGGGCGCTT CCCCAGGAGA GGGACCAGGG	2760
	GTGCGCCAC AGCCTGCTCC ATTCTCCAGT CTGAACAGTT CAGCTACAGT CTGACTCTGG	2820
20	ACAGGGGGTT TCTGTTGCAA AAATACAAAA CAAAAGCGAT AAAATAAAG CGATTTTCAT	2880
	TTGGTAGGCG GAGAGTGAAT TACCAACAGG GAATTGGGCC TTGGGCTATG CCATTTCTGT	2940
	TGTAGTTTGG GGCAGTGCAG GGGACCTGTG TGGGGTGTA ACCAAGGCAC TACTGCCACC	3000
25	TGCCACAGTA AAGCATCTGC ACTTGACTCA ATGCTGCCCG AGCCCTCCCT TCCCCCTATC	3060
	CAACCTGGGT AGGTGGGTAG GGGCCACAGT TGCTGGATGT TTATATAGAG AGTAGGTGA	3120
30	TTTATTTTAC ATGCTTTTGA GTTAATGTTG GAAAACTAAT CACAAGCAGT TTCTAAACCA	3180
	AAAAATGACA TGTGTAAAA GGACAATAAA CGTTGGGTCN AAATGGGWRA AAAAAAAAAA	3240
35	AAAAAAGGGG GGCCCCCTCTA AAGNNCCANN CTTCGT	3276

## (2) INFORMATION FOR SEQ ID NO: 292:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

	TTGCAATGGT TGAATTCCCC TCCTCACGCC AGCCTAGGAG AAGAAGTTGG TAGTCCCAGA	60
50	GGTGAGGCAG GAGGCGGCAG TTTCTGGCGG GTGAGGGCGG AGCTGAAGTG ACAGCGGAGG	120
	CGGAAGCAAC GGTCGGTGGG GCGGAGAAGG GGGCTGGCCC CAGGAGGAGG AGGAAACCCCT	180
55	TCCGAGAAAA CAGCAACAAG CTGAGCTGCT GTGACAGAGG GGAACAAGAT GCGGGCGCCG	240
	AAGGGAGCCT CTGGGTGAGG ACCCAACTGG GGCTCCCCCG GCTGCTGCTG CTGACCATGG	300
60	CCTTGGCCCG AGGTTCGGGG ACCGCTTCGG CTGAAGCATT TGACTCGGTC TTGGGTGATA	360

	CGGCGTCTTG CCACCGGGCC TGTCA GTTGA CCTACCCCTT GCACACCTAC CCTAAGGAAG	420
	AGGAGTTGTA CGCATGTCAG AGAGGTTGCA GGCTGTTTTT AATTGTGTCAG TTTGTGGATG	480
5	ATGGAATTGA CTTAAATCGA ACTAAATTGG AATGTGAATC TGCATGTACA GAAGCATATT	540
	CCCAATCTGA TGAGCAATAT GCTTGCCATC TTGGTTGCCA GAATCAGCTG CCATTGCTG	600
10	AACTGAGACA AGAACAAC TTATGCCCTGA TGCCAAAAAT GCACCTACTC TTTCTCTTAA	660
	CTCTGGTGAG GTCATTCTGG AGTGACATGA TGGACTCCGC ACAGAGCTTC ATAACCTCTT	720
	CATGGACTTT TTATCTTCAA GCCGATGACG GAAAAATAGT TATATTCCAG TCTAAGCCAG	780
15	AAATCCAGTA CGCACCACAT TTGGAGCAGG AGCCTACAAA TTTGAGAGAA TCATCTCTAA	840
	GCAAAATGTC CTATCTGCAA ATGAGAAAT CACAAGCGCA CAGGAATTTT CTTGAAGATG	900
20	GAGAAAGTGA TGGCTTTTTA AGATGCCTCT CTCTTAACTC TGGGTGGATT TTAAC TACAA	960
	CTCTTGCTCT CTGGTGATG GTATTGCTTT GGATTGTGTG TGCAACTGTT GCTACAGCTG	1020
	TGGAGCAGTA TGTCCCTCT GAGAAGCTGA GTATCTATGG TGACTTGGAG TTTATGAATG	1080
25	AACAAAAGCT AACAGATAT CCAGCTTCTT CTCTGTGGT TGTAGATCT AAAACTGAAG	1140
	ATCATGAAGA AGCAGGGCCT CTACCTACAA AAGTGAATCT TGCTCATCTT GAAATTTAAG	1200
30	CATTTTCTTT TTAAGAGACA AGTGAATAG ACATCTAAAA TTCCACTCCT CATAGAGCTT	1260
	TTAAATGGT TTCATTGGAT ATAGGCCTTA AGAAATCACT ATAAATGCA AATAAAGTTA	1320
	CTCAAACTCG TGAAGACTGT ATTTGCTATA ACTTTATGG TATGTTTTT GTAGTAATTT	1380
35	AAGAGGTGGA TGTITGGGAT TGTATTATTA TTTTACTAAT ATCTGTAGCT ATTTGTTTTT	1440
	TGCTTTGGT TATGTTTTTT TTCCCTTTTC TTAGCTATGA GCTGATCATT GCTCCTTCTC	1500
40	ACCTCCTGCC ATGATACTGT CAGTTACCTT AGTTAACAAG CTGAATATTT AGTAGAAATG	1560
	ATGCTTCTGC TCAGGAATGG CCCACAAATC TGTAAATTGA AATTAGCAG GAAATGACCT	1620
	TTAATGACAC TACATTTTCA GGAAGTGAAT TCATTAAAAT TTTATTGAA TAATTAAAAA	1680
45	AAAAAAAAA AANCT	1695

50 (2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

60 CACTTTCAGC AGTCCTTTGC TCTCTTTGCT TCTACCTCAA ATAGCCCCAG GAGTGGGCTT 60

	TAGTCTCCAA TATGGAGCAT CTCAAGCTTC TCCTGGGGGA TGGGGATTGG GATGGGCAGA	120
5	ATCTGTTTTG GWTCTCCGGG TTATTTCCAG TGGGTGTAAA AGCAGAGCTG GGCCTTTCCC	180
	TCTCTTATCC CTGAGGGTGG GTAAGAAGGA CTGTATCTAC ACCTGTTCTT CCCTACCTTC	240
	TCTTTTGTTA GGGAGGCCTC ATTCTAAGTT CCTCAAGAGA GTCCTTGGCT TAAAGCTGTA	300
10	GCAAGGGTGT GCTAGGTGGG GGATTTGGAG CAAAACCGTC GAGTAGGCAT GATACTGGTA	360
	TGGAGTGGGC CTGCAAAATC AGACAGAAAT GGCTTGAGAA GCCGCAGGGG AGCATGCCTG	420
15	TCTCTCAGTG ATAGAGTATG GGAGGGACCT CCCTAGCTTG GAAAATGAGA ATTGAAGGGG	480
	TTATGAACAA ATAGGATGCC TAGTTGAGGA TGTTCCTCAA GTTTTGTTCCA ATCTTATCAT	540
	TAGTAGATTT TATAAGCCAC AGAGACAAAC CAGAAACGGA ATAATGTTAC TTTGGATGCT	600
20	TTATTTTTTT GTTCTAGGTG TGGCTTTGTA CATGCAGAAG AATGCTATAT GCTGCACATT	660
	TTGCCTTTAA AGTCTTACGA CTTTCCCAT TTTAGTCTAA TGGGAAGATA CAGATGTGCA	720
25	AGTCTGCTTT TTTGTTTTTT GTTATTATTT TTTTTTTTTT GCTCTGTGTT ATGGACATTT	780
	TCAGACATGC ACAGAAGTGG AGAGGATGGT CCTTGGACCC MATGTGTCCA TCACCTAGCT	840
	GCATCACTTA TCAGCTATGG TCAACCTGGT TTCATCTGTA TCTCTCTCTT TTCACCTGTA	900
30	TTGTTTTATTG AAAATCCAAG ACACTATGCC AATGCAACCG TGA CTACTTT GGGAGATTGG	960
	TAGTCTCTTT TGATGGTGAT AGTGATGGG TGCATATCA TAATCACATC AGGTCTGCTT	1020
35	TTTGCTTTTA ATGTTAACTA ATGAAGTTC AGAGATGGGC CTTAGAAATG TGTTTTAAGA	1080
	ATTAACAAGG AGTCTCAAAA AGAAATGAGA GGGATGCTTC CTTTNCCTT GCATCTACAA	1140
	AACMAGAGAG AGACTGTTCT GTTGTAAC TCTTCAAAA ATTCTGATAT GGTAAAGTAC	1200
40	TTGAGACCTT TCACCAGAAT GTCAATCTTT TTTCTGTGT AACATGGAAA CTGTGTGAC	1260
	CATTAGCATT GTTATCAGCT TGTACTGGTC TCATAACTCT GGTTTTGGAA GAATAATTG	1320
45	GAAATTGTTG CTGTGTTCTG TGAAAATAAC CTCCTCAAAA TAATTAGTAA CTGGTTGTTT	1380
	TACTTGGTAA TTTGACACCC TGTTAATAAC GCAATTATTT CTGTGTTCTT AACAGTATA	1440
	AATAGTTGTA AGTTTGCATG CATGATGGAA AAATAAAAAC CTGTATCTCT GTTAAAAAAA	1500
50	A	1501

55 (2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

5	TGANTGTGGT CCCGGGTGCN GATTGGCAGN GCCTCCGCCG CGGCTCGTGG TTGTCCCGCC	60
	ATGGCACTGT CGCGGGGGCT GCCCCGGGAG CTGGCTGAGG CGGTGGCCGG GGGCCGGGTR	120
	CTGGTGGTGG GGGCGGGCGG CATCGGCTGC GAGCTCCTCA AGAATCTCGT GCTCACC GG	180
10	TTCTCCACACA TCGACCTGAT TGATCTGGAT ACTATTGATG TAAGCAACCT CAACAGACAG	240
	TTTTTGTTC AAAAGAAACA TGTGGAAGA TCAAAGGCAC AGGTGCCAA GGAAAGTGTA	300
15	CTGCAGTTTT ACCCGAAAGC TAATATCGTT GCCTACCATG ACAGCATCAT GAACCCTGAC	360
	TATAATGTGG AATTTTTCCG ACAGTTTATA CTGGTTATGA ATGCTTTAGA TAACAGAGCT	420
	GCCCGAAACC ATGTTAATAG AATGTGCCTG GCAGCTGATG TTCCTCTTAT TGAAAGTGGA	480
20	ACAGCTGGGT ATCTTGACA AGTAACTACT ATCAAAAAGG GTGTGACCGA GTGTTATGAG	540
	TGTCATCCTA AGCCGACCCA GAGAACCTTT CTGGCTGTA CAATTCGTAA CACACCTTCA	600
25	GAACCTATAC ATTGCATCGT TTGGCAAAG TACTTGTTC ACCAGTTGTT TGGGAAGAA	660
	GATGCTGATC AAGAAGTATC TCCTGACAGA GCTGACCTG AAGCTGCCTG GGAACCAACG	720
	GAAGCCGAAG CCAGAGCTAG AGCATCTAAT GAAGATGGTG ACATTAAACG TATTTCTACT	780
30	AAGGAATGGG CTAAATCAAC TGGATATGAT CCAGTTTAAA CTTTTTACCA AGCTTTTTTA	840
	AGATGACATC AGGTATCTGT TGACAATGGA CAACTATGG CGGAAAAGGA AACCTCCA	900
35	TCCGTGGAC TGGGCTGAAG TACAAAGTCA AGGAGAAGAA ACGAATGCAT CAGATCAACA	960
	GAATGAACCC CAGTTAGGCC TGAAAGACCA GCAGGTTCTA GATGTAAAGA GCTATGCACG	1020
	TCTTTTTTCA AAGAGCATCG AGACTTTGAG AGTTCATTTA GCAGAAAAGG GGGATGGAGC	1080
40	TGAGCTCATA TGGGATAAGG ATGACCCATC TGCAATGGAT TTTGTACCT CTGCTGCAA	1140
	CCTCAGGATG CATATTTTCA GTATGAATAT GAAGAGTAGA TTTGATATCA AATCAATGGC	1200
45	AGGGAACATT ATTCTGCTA TTGCTACTAC TAATGCAGTA ATTGCTGGGT TGATAGTATT	1260
	GGAAGGATTG AAGATTTTAT CAGGAAAAAT AGACCAGTGC AGAACAAATT TTTTGAATAA	1320
	ACAACCAAAC CCAAGAAAGA AGCTTCTTGT GCCTTGTCGA CTGGATCCTC CCAACCCCAA	1380
50	TTGTTATGTA TGTGCCAGCA AGCCAGAGGT GACTGTGCGG CTGAATGTCC ATAAAGTGAC	1440
	TGTTCTCACC TTACAAGACA AGATAGTGAA AGAAAAATTT GCTATGGTAG CACCAGATGT	1500
55	CCAAATGAA GATGGGAAAG GAACAATCCT AATATCTTCC GAAGAGGGAG AGACGGAAGC	1560
	TAATAATCAC AAGAAGTTGT CAGAATTTGG AATTAGAAAT GGCAGCCGGC TTCAAGCAGA	1620
60	TGACTTCCTC CAGGACTATA CTTTATGAT CAACATCCTT CATAGTGAAG ACCTAGGAAA	1680

	GGACGTTGAA TTTGAAGTTG TTGGTGATGC CCCGAAAAA GTGGGSSCCA AACAAGCTGA	1740
	AGATGCTGCC AAAAGCATAA CCAATGGGCA GTGATGATGG AGCTCAGCCC TCCACCTCCA	1800
5	CAGCTCAAGA GCAAGATGAC GTTCTCATAG TTGATTGCGA TGAAGAAGAT TCTTCAAATA	1860
	ATGCCGACGT CATGAAGAAG AGAGAAGCCG CAAGAGGAAA TTAGATGAGA AAGAGAATCT	1920
10	CAGTGCAAAG AGGTCACGTA TAGAACAGAA GGAAGAGCTT GATGATGTCA TAGCATTAGA	1980
	TTGAACAGAA ATGCCTCTAA ACAGAACCCT CTTACTATTT AGTTTATCTG GGCAGAACCA	2040
	GATTGTTATG TCCTTTGTTC CAAAGGAAA AAATTGACAG CAGTGACTTG AAAATGATTG	2100
15	TGCTCCCTTT GAAAGCATTC ATTTTGCTAG AACTGTTAGA CACATTGCAG TATGCTGTAT	2160
	TGAAAGTAGG AATATAGTTT TAAAAACCCT TTGAACAAAG TGTGTGCATA ACCAGTCATG	2220
20	AGATAAAACA ACACAAATGA TGTTCCTTTT TTAATGTAAA TACCCTTAGG TATCATTAAT	2280
	AGTTTCAAAA TATTGTGGTT TAGTAAAGTT GATACCTGGT TATAAATATT ATGCCTTTAT	2340
	TTTTGGCTAG AAGAAGAATT ATTTTTAGCC TAGATCTAAC CATTTTCATA CTCTTAACTG	2400
25	ATTGAAACAG ATTCAAAGAA GTATCGAGTG CTATGCATTG AAAGTTGTTT TTAAATGTTA	2460
	GATGGCACTA TGTATATTAA TGTAACAAAC TGTAAATTTA CTCAAGTTTT CAGTTGTAC	2520
30	CGCTGGTAT GTCTGTGTAA GAAGCCAATT TTTGTGTATT GTTACAGTTT CAGGTTATTT	2580
	ATATTGATG TTTTGTAAAA CTCAAATAAC GACTATACTT ATGGACCAAA TAAATGGCAY	2640
	TGCATTCTKG TKAAAAAAN NACAGAAAAA AAAAAAACA AGA	2683

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(2) INFORMATION FOR SEQ ID NO: 295:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1454 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

	GGACTCGGGG TGGCTCTAAG GGGCAGGAT AGGCTGGGG AGCGCCGGCC TGTGGCCCTG	60
50	ACCAGCCCTT TCTCGTGAG GTTCCACCCC GATGCAGGTG GTCACGTGCT TGACCGGGA	120
	CAGCTACCTG ACGCACTGCT TCCTCCAGCA CCTCATGGTC GTGCTGTCTT CTCTGGAACG	180
55	CAGGCCCTCG CCGGAGCCTG TTGACAAGGA CTTCTACTCC GAGTTTGGGA ACAAGACCAC	240
	AGGGAAGATG GAGAACTACG AGCTGATCCA CTCTAGTCGC GTCAAGTTTA CCTACCCAG	300
	TGAGGAGGAG ATTGGGGACC TGACGTCAC TGTGGCCCAA AAGATGGCTG AGCCAGAGAA	360
60	GGCCCCAGCC CTCAGCATCC TGCTGTACGT GCAGGCCTTC CAGGTGGGCA TGCCACCCCC	420



	TGGGTGCTGC AGGGGCCCC TGCGCCCCAA GACACTCCTG CTCACCAGCT CCGAGATCTT	480
5	CCTCCTGGAT GAGGACTGTG TCCACTACCC ACTGCCCAG TTTGCCAAAG AGCGCCGCA	540
	GAGAGACAGG TACCGGCTGG ACGATGGCCG CCGCGTCCGG GACCTGGACC GAGTGCTCAT	600
	GGGCTACCAG ACCTACCCGC AGCCCTCACC CTCGTYTTCG ATGACGTGCA AGGTCATGAC	660
10	CTCATGGCA GTGTACCCCT GGACACTTT GGGGAGGTGC CAGGTGGCCC GGCTAGAGCC	720
	AGCCAGGGCC GTGAAGTCCA GTGGCAGGTG TTTGTCCCCA GTGCTGAGAG CAGAGAGAAG	780
	CTCATCTCGC TGTGGCTCG CCAGTGGGAG GCCCTGTGTG GCCTGAGCTG CCTGTGAGC	840
15	TCACCGGCTA GCCCAGGCCA CAGCCAGCCT GTCGTGTCCA GCCTGACGCC TACTGGGGCA	900
	GGGCAGCAGG CTTTGTGTGT CTCTAAAAAT GTTTTATCCT CCCTTTGGTA CCTTAATTG	960
20	ACTGTCTCG CAGAAATGTG AACATGTGTG TGTGTGTGT TAATTCTTTC TCATGTTGGG	1020
	AGTGAGAATG CCGGGCCCCCT CAGGGCTGTT CGGTGTGCTG TCAGCCTCCC ACAGGTGGTA	1080
	CAGCCGTGCA CACCAGTGTG GTGTCTGCTG TTGTGGGACC GTTGTTAACA CGTGACACTG	1140
25	TGGGTCTGAC TTTYTCTTCT ACACGTCCTT TCCTGAAGTG TCGAGTCCAG TCCTTTGTG	1200
	CTGTGTGCTG TGCTGTGCT GTGCTGTG GCATCTTGCT GCTAATCCTG AGGCTGGTAG	1260
30	CAGATGCAC ATTGGAAGCT CCCACCCAT ATTGTTCTTC AAAGTGGAGG TCTCCCCTGA	1320
	TCCAGACAAG TGGGAGAGCC CGTGGGGCA GGGGACCTGG AGCTGCCAGC ACCAAGCGTG	1380
	ATTCTGCTG CCTGTATTCT CTATTCCAAT AAAGCAGAGT TTGACCCGW MAAAAAAAAA	1440
35	AAAAAAAAA AACN	1454

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(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

50

ACCTTGGCAT GCCCACAAA CAGATCACCA GCCAGCTTAC ACAGGCATTA ACTCTCCTCA	60
ATGAGGAAGA ATCATTCACA ACTGAGCAAG ACATTCATAT GATCATTTAA GGAAGTGT	120
55 CCCTTATGTG TTAGCAAGTA TAATCGGCTA ACTCCTAAAT CCCAATGAAT AGTCCTAGGC	180
TGGACAGCAA TGGGCTGCAA TTAGGCAGAT AAAGACATCA GTCCAGTAA ATGAATCCAT	240
60 AGACTCATCT AGCACCAACT ACCATTAGCA CTATGTTAGG AGCTGCAAGG CCCCAAAGTA	300

GAAGATGTGC ATAATGTCTG CTCTGTGTGA GCTCAGGAGA CAATTCAGC ACAGACACTA 360  
 CAGTTAACGC TGAAGTCAG CTGCAAGTAA TAGCAWGAAC AGTCAGAAAA ATACCTTATG 420  
 5 AGGGGGCAGG GCTGAAGCTG GGCCTTGAAG GATGGATGAA ATTTGGATAG AGAATGAGGA 480  
 AGACAGAGGG NCTCCAAGTG AGAGAAGCAT GAAAAATGAG CARGGGCCTG GATCAGTGGG 540  
 GTGTATTTCAG AGCACCTYTC CAGATGCACC ATGCATGCTC ACAGTCCCTT GCCTATGTGT 600  
 10 GGCAGAGTGT CCCAGCCAGA TGTGTGCCCC CACCCCATGT CCATTTACAT GTCCTTCAAT 660  
 GCCCACCTCA AAAGGYACYT CTTCTGTAAA GCTTTCCCTK GGTATCAGGA ATCAAAATTA 720  
 15 ATCAGGGATC TTTTCACACT GCTGTTTTTT CCTCTTTGGT CCTTCTATCA CTAAACTCA 780  
 TCTCATTTCAG CTTACAGCA TAACTAATTA TTTGTTTTCC TCACTACA 828

20

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 2416 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

TCAATTTCCA TTAAGTCAGA TCAGCCATG TGATTCACCA TTTGTGAGG TCTCAGGTTT 60  
 AACAAAACCT ACTATCACCA TCATCCTTCA ACAGCCACAG TCTGAATTGA GCCAACATTT 120  
 35 TTTTTCCTTT GAGAAAGAAG TGGACTGGGG CACAACTTTT AGTCTGAGGG GAGCTAGTGG 180  
 AAATCTAGAC AATAGAAGTC ATCGATAGCA GCTTTTCCTC AAATGTGTGA CTCCTCAGGG 240  
 40 GCTAAACTGC TCTTAGCTTA GAATTATGCT TTAGTAGAGA TCTAGCAGAT AAGTGGGTTA 300  
 ATCACTACCA TCCTGTAAGT AGTTATATAG CTTCCAGACA TGAGGGAGAC ATCAAAACAGG 360  
 GATGGAAGCA ACCCCAAGGA TATGCAAGAA GGCATGATG AACCCCTTC CCTCTGGCAG 420  
 45 GAGAACAAGG CCAACCAAGG GACAGACTGG AAAGCACTTA GATGTTTAAG GAGGAGAAAG 480  
 GGGAAAGCTT GACCAGTCTT TGCTTTTTCG CAAGTTCAGC CAGTTCTCCG CTGCTTGCAA 540  
 50 CCTCTAGCGC AGTAACATTT GCAGAATTGC AGATTTTCCC CCAGATACTA GGAGGAAAGG 600  
 GACTTTGGGG GGTGGGAAG GGGTCGTGGT GTTTTAAAAG CATAAGTTAC CTGTTTGCAC 660  
 TGTMTAAGA TAGGAAAAAA AAATAGTGGG CAAGGTGAAC ATCAGACGTA AATTGTGTG 720  
 55 TTTTATTTT GTCATGCTCT TGAAAATGTT TGACCATTTG TAGTATACAC AGTGAAACTT 780  
 GATTCCTCTG TGCATAAAAC ACTATATTTT TTTGGAAATG TTAGTGTCCA AAAGCCTCTT 840  
 60 CCCTCCCTTT CTTTTCCTA TGTACTTCCT TCATACTGTC TTTACTGATC AGCCAGGCAA 900

	TAGCCATCCA AGAGCTAGAG CATGAAACAG GGCCCTTTCC AAGTAGGCTC TGGGTGTCCT	960
5	AAGCCAGCGT GTGCCCTCTG GTTTAGTGAG TGTAAATAGAG TCCCTGGCAC CTTTCTTTGC	1020
	AAATGAGGCT AACAGACCAG ACTGCAGCAA GTTATCAGAT TCCTCAATCA GATGCACTAG	1080
	GAGTGAGGAG CCCAGGGATG GAGGGGGTTC CTGAAGTATT GCAGTTGGCT GTAGTAGCTG	1140
10	AGTTCTTTTC CATGTTACCG AAACGTAGC CAGTTACAGT TTA CT CAGGA AAACGGTAGA	1200
	TCAATTCAGC CATGGTAGTG CTGGTTGGCA GGGATTGGTA ACGGAGAGAA CTGCTCATCA	1260
15	GCCAAAAC TC AAGCCTTGCC TTTTAGGAGG CCACCAGCAG AGGGACTTGG TCCTCCTTGT	1320
	CTGGTACTTG TGTACATGCC GGTGACCTGA GGACTCCACT CACACTGGCG AGCAAAAAGG	1380
	GAGCAGTGAT TCTCTTTTCT CTCCCCACCC CCTGCCCTTT GTTACCAACA CCAGTTTCCC	1440
20	AGGGGTACA TGAGTTCTG AATTTTAAA AAATGTTTTT GGTITGGTIT TTCTGGGGAC	1500
	TGATAAGTGC TTAAAGCAAT GTCCATACCC CGTCAAGACT CCCAGCTTAG TCATTTTCTT	1560
25	GTATTTTCT GTTCACAGTA TTTGTGTGTG TGCTTGTITT GGCAGCTCAT TTTGGCTGTA	1620
	TTATATATTG AGTGATGAAT TGATCCTCTT TTTTCCCTAA GGGATATGAA TTGTTTCT	1680
	TGTGTATAT TCTGCTGTG AATAGCTGA GCAAACCTGG GGCTGACACG CGTAAGSTAG	1740
30	GGCTGCAAA CGAGAAGAGA CCCGGTGGAG TGTACTTGTG CCTGACAGGC TGACCTACCT	1800
	GAGTCTCTGA GCTTTTTCAGT CCAAATCTTT GCAAGGCTCA AAATGCCACA GAACCTCTCC	1860
35	TCTTCTCCCC ACTCCCCATG GCAGGGACCG GACCATCCCT ACATGCAACA TGCTGTTCTT	1920
	CCAGCCCCTC CCATTGCCAT GGCAAAACAG GTACCTTTGG GGCATGGGG CATTACATGG	1980
	GATGCTTGTG TAATCGACCA CCTAGCCTTC TCTCTCCCT CCCGTCTCC CCCAGAATCA	2040
40	CTTCTAGGA CACCCGAGCT GCTTGCCAG GTCCTGTTT CCCTGCTAAC TCCAGAGAAG	2100
	CATCCAGGG CTTTGTGACA GTCTCTAATT CCCTTCCCT CTCGTTAAGA ATCATATTGT	2160
45	ATAGTAGCTT TCAGACCATA CAGTATTCAT TGGGTACTC CTATTATTAT CAAGTAGCTG	2220
	GAATGTGAA GTTCGGAGTA GTTAGATCTT TAGCTTTTAT TCCTTATTTT TTTGTATTAC	2280
	TCTCCATGTG TATAAATTAT TGATCATGTT GCTGGCTTTT ATAACTCTA AGCGAAGGAG	2340
50	GAGCACTGCC TCAGCCTTTG CACATGGTAA TGAAGCACTG TTTTAAATA AAAGRGRGAA	2400
	MCMCAAAAA AAAAA	2416
55		

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 base pairs

60

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

	GAATTCGGCA CGAGCCATGC YTGCCCTCTC CTGTGATCTT ACAGTCACIT TGTGGCTGT	60
	TTCTGACTCA GCAGCTACCT GCATTGTGGC CAAAGGATGA CCTATTCCTT CTCAGGAGGG	120
10	CAAAAATGTG GAATAGTGTG TGTCCATGCC TCTCCTCATG GGCTACCACC TCTGCCACCG	180
	TGGTTAATCA GTAACAACCA GGAGAGAAGC TGCTGGAAC TACCTCTGGG AACTCCCTGG	240
15	ATGGTTTGGT GCAGGAATGT AGTAGGCATA CACGTGGTTG CGTGGATCTG GGCCCTCCTG	300
	ATGTGAGTAG AGAGGTAAAA GGSCACCATC TCCTTGACCT YTGCGGAAC TATCCACAAA	360
	GAAGATGTTT CCAAGATGCT TCTGAAGATT GSCTAAAAAT AGCCGGTTTC CACCCCGTG	420
20	AATGCATCCA TTCTAGAATG CTCCTTCACC AGGACCAGAG AACTGATTTA CAGAAGTGAC	480
	ATGAAAACAT TCCATCCCAG AATTGTCANT ACCTCAAATT NAATTTCTAC CTATTAAAAA	540
25	NAAAA	545

30 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1530 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

40	GGCTCTGCTG GGCATCATAC TTGTCACTGG GTAAACAGTT TGCCCACTTA CCGCAGATGA	60
	AGCTGCTTGC CAGGGCTCTC CGGCTCTGTG AGTTTGGGAG GCAGGCATCT TCCAGGAGGC	120
	TGGTGGCTGG CCAGGGATGT GTGGGGCCCC GCGGAGGGTG CTGGCTCCC GTCCAGGTGG	180
45	TTGGGCCCAG GGCTGATCTC CCACCTGTG GAGCCTGCAT TACTGGAAGG ATCATGCGGC	240
	CAGATGATGC CAACGTGGCC GGCAATGTCC ACGGGGGGAC CATCCTGAAG ATGATCGAGG	300
50	AGGCAGGCGC CATCATCAGC ACCCGGCAIT GCAACAGCCA GAACGGGGAG CGCTGTGTGG	360
	CGGCCCTGGC TCGTGTGAG CGCACCGACT TCCTGTCTCC CATGTGCATC GGTGAGGTGG	420
	CGCATGTICAG CGCGGAGATC ACCTACACCT CCAAGCACTC TGTGGAGGTG CAGGTCAACG	480
55	TGATGTCCGA AAACATCCTC ACAGGTGCCA AAAAGCTGAC CAATAAGGCC ACCCTGTGGT	540
	ATGTGCCCC TGCCTGAAG AATGTGGACA AGGTCTCGA GGTGCCTCCT GTTGTGTATT	600
60	CCCGGCANGA GCAGGAGGAG GAGGGCCGGA AGCGGTATGA AGCCAGAGG CTGGAGCGCA	660

	TGGAGACCAA GTGGAGGAAC GGGGACATCG TCCAGCCAGT CCTCAACCCA GAGCCGAACA	720
5	CTGTCAGCTA CAGCCAGTCC AGCTTGATCC ACCTGGTGGG GCCTTCAGAC TGCACCTGTC	780
	ACGGCTTTGT GCACGGAGGT GTGACCATGA AGCTCATGGA TGAGGTGCCC GGGATCGTGG	840
	CTGCACGCCA CTGCAAGACC AACATCGTCA CAGCTTCCGT GGACGCCATT AATTTTCATG	900
10	ACAAGATCAG AAAAGGCTGC GTCATCACCA TCTCGGGACG CATGACCTTC ACGAGCAATA	960
	AGTCCATGGA GATCGAGGTG TTGGTGGACG CCGACCTGT TGTGGACAGC TCTCAGAAGC	1020
15	GCTACCGGGC CGCCAGTGCC TTCTTCACCT ACGTGTGCT GAGCCAGGAA GGCAGGTCCG	1080
	TGCCTGTGCC CCAGCTGGTG CCCGAGACCG AGGACGAGAA GAAGCGCTTT GAGGAAGGCA	1140
	AAGGGCGGTA CTGTCAGATG AAGGCGAAGC GACAGGGCCA CGCGGAGCCT CAGCCCTAGA	1200
20	CTCCCCTCTC TGCCACTGG TGCCTGAGT AGCCATGGCA ACGGGCCCAG TGTCCAGTCA	1260
	CTTAGAAGTT CCCCCCTGG CCAAAAACCC AATTACATT GAGAGCTGGT GTTGTCTGAA	1320
25	GTTTTCTGAT CACAGTGTA ACCTGTACTC TCTCTGCAA ACCTACACAC CAAAGCTTTA	1380
	TTTATATCAT TCCAGTATCA ATGCTACACA GTGTTGTCCC GAGCGCCGGG AGGCGTTGGG	1440
	CAGAAACCCT CGGAATGCT TCCGAGCAG CTGTAGGTA TGGGAAGAAC CCAGCACCAC	1500
30	TMATAAAGCT GNTGCTTGGC TGGGAAGNA	1530

35 (2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 997 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

45	AGGTAGTGAG AGACACATTA CACCTAACCA ACAAGAAGAA GGATCCTCCC CCTTATAATT	60
	TAACTATGTT TACAGGGAAT GCGTACATTG TGGCTTCCCG AGNATTTCTG CCAACATGTT	120
	TTGAAGAACC CTAAATCCCA ACAACTGATT GAATGGGTAA AAGACACTTA TAGCCCAGAT	180
50	GAACACCTCT GGGCCACCCT TCAGCGTGCA CGGTGGATGC CTGGCTCTGT TCCCAACCAC	240
	CCCAAGTACG ACATCTTCAG ACATGACTTC TATTGCCAGG CTGGTCAAGT GGCAGGGTCA	300
55	TGAGGAGAC ATCGATAAGG GTGCTCCTTA TGCTCCCTGC TCTGGAATCC ACCAGCGGGC	360
	TATCTGCGTT TATGGGGCTG GGGACTTGAA TTGGATGCTT CAAAACCATC ACCTGTGGC	420
60	CAACAAGTTT GACCCAAGG TAGATGATAA TGCTCTTCAG TGCTTAGAAG AATACCTACG	480

TTATAAGGCC ATCTATGGGA CTGAACCTTG AGACACACTA TGAGAGCGTT GCTACCTGTG 540  
 GGGCAAGAGC ATGTACAAAC ATGCTCAGAA CTGCTGGGA CAGTGTGGGT GGGAGACCAG 600  
 5 GGCTTTGCAA TTCGTGGCAT CCTTTAGGAT AAGAGGGCTG MTATTAGATT GTGGGTAAGT 660  
 AGATCTTTTG CCTTGCAAAT TGCTGCCTGG GTGRATGCTG CTGTCTCTCT CACCCCTAAC 720  
 10 CCTAGTAGTT CCTCCACTAA CTTTCTCACT AAGTGAGAAT GAGAACTGCT GTGATAGGGA 780  
 GAGTGAAGGA GGGATATGTG GTAGAGCACT TGATTTCAGT TGAATGCCTG CTGGTAGCTT 840  
 TTCCATCTG TGGAGCTGCC GTTCCTAATA ATTCCAGGT TGGTAGCGTG GAGGAGAACT 900  
 15 TTGATGGAAA GAGAACCTTC CCTTCTGTAC TGTTAACCTA AAAATAAATA GCTCCTGATT 960  
 CAAAGTAAGG AAAAAA AAAAGAAAAA AACTCGA 997

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(2) INFORMATION FOR SEQ ID NO: 301:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2345 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

TTGAGGCCGA CGCTAGGGGC CCGGAAGRAA ACTGCGAGGC GAAGTGACC GGGGACCGAG 60  
 CATTTTCAGAT CTGCTCGGTA GACCTGGTGC ACCACCACCA TGTTCGGCTGC AAGGCTGGTG 120  
 35 TGTCCTCGGA CACTACCTTC TAGGGTTTTT CACCCAGCTT TCACCAAGGC CTCCTCTGTT 180  
 GTGAAGAATT CCATCACGAA GAATCAATGG CTGTTAACAC CTAGCAGGGA ATATGCCACC 240  
 40 AAAACAAGAA TTGGGATCCG GCGTGGGAGA ACTGGCCAAG AACTCAAAGA GGCAGCATTG 300  
 GAACCATCGA TGGAAAAAAT ATTTAAAATT GATCAGATGG GAAGATGGTT TGTTCCTGGA 360  
 GGGGCTGCTG TTGGTCTTGG AGCATTTGTC TACTATGGCT TGGACTGTC TAATGAGATT 420  
 45 GGAGCTATTG AAAAGGCTGT AATTTGGCCT CAGTATGTCA AGGATAGAAT TCATTCCACC 480  
 TATATGTA CTAGCAGGGAG TATGGTTTA ACAGCTTTGT CTGCCATAGC AATCAGCAGA 540  
 50 ACGCCTGTTT TCATGAACCT CATGATGAGA GGCTCTTGGG TGACAATTGG TGTGACCTTT 600  
 GCAGCCATGG TTGGAGCTGG AATGCTGGTA CGATCAATAC CATATGACCA GAGCCACGGC 660  
 CCAAAGCATC TTGCTTGGTT GCTACATTCT GGTGTGATGG GTGCAGTGGT GGCTCCTCTG 720  
 55 ACAATATTAG GGGGTCCTCT TCTCATCAGA GCTGCATGGT ACACAGCTGG CATGTGGGA 780  
 GGCTCTCCA CTGTGGCCAT GTGTGCGCCC AGTGAAAAGT TTCTGAACAT GGGTGCACCC 840  
 60 CTGGGAGTGG GCCTGGGTCT CGTCTTTGTG TCCTCATTGG GATCTATGTT TCTTCCACCT 900

	ACCACCGTGG CTGGTGCCAC TCTTTACTCA GTGGCAATGT ACGGTGGATT AGTTCTTTTC	960
5	AGCATGTTCC TTCTGTATGA TACCCAGAAA GTAATCAAGC GTGCAGAAGT ATCACCAATG	1020
	TATGGAGTTC AAAAATATGA TCCCATTAAC TCGATGCTGA GTATCTACAT GGATACATTA	1080
	AATATATTTA TGGCAGTTGC AACTATGCTG GCAACTGGAG GCAACAGAAA GAAATGAAGT	1140
10	GACTCAGCTT CTGGCTTCTC TGCTACATCA AATATCTTGT TTAATGGGGC AGATATGCAT	1200
	TAAATAGTTT GTACAAGCAG CTTTCGTTGA AGTTTAGAAG ATAAGAAACA TGTCATCATA	1260
	TTTAAATGTT CCGGTAATGT GATGCCTCAG GTCTGCCTTT TTTTCTGGAG AATAAATGCA	1320
15	GTAATCCTCT CCCAAATAAG CACACACATT TTCAATTCTC ATGTTTGAGT GATTTTAAAA	1380
	TGTTTTGGTG AATGTGAAAA CTAAAGTTTG TGTCATGAGA ATGTAAGTCT TTTTTCTACT	1440
20	TTAAATTTA GTAGGTTTAC TGAGTAACTA AAATTTAGCA AACCTGTGTT TGCATATTTT	1500
	TTTGGAGTGC AGAATATTGT AATTAATGTC ATAAGTGATT TGGAGCTTTG GTAAAGGGAC	1560
	CAGAGAGAAG GAGTCACCTG CAGTCITTTG TTTTTTTAAA TACTTAGAAC TTAGCACTTG	1620
25	TGTTATTGAT TAGTGAGGAG CCACTAAGAA ACATCTGGGT ATTTGGAAAC AAGTGGTCAT	1680
	TGTTACATTC ATCTGCTGAA CTTAACAAAA CTGTTTCATCC TGAACAGGC ACAGGTGATG	1740
30	CATTCCTCTG CTGTGCTTC TCAGTCTCT CTTCCTCAATA TAGATGTGGT CATGTTTGAC	1800
	TTGTACAGAA TGTTAATCAT ACAGAGAATC CTGTATGGAA TTATATATGT GTGTTTTACT	1860
	TTTGAATGTT ACAAAGGAA ATAACTTTAA AACTATTCTC AAGAGAAAAT ATTCAAAGCA	1920
35	TGAAATATGT TGCTTTTTCC AGAATACAAA CAGTATACTC ATGATTGCTA AGTGTTTTTT	1980
	TATTTTTGCA TATTTATTGA ACTGTCTAAT TGAATACAGC TTGCTCTTGT CACCTCTTCA	2040
40	AGCTTTCAG CCTTTATAGA AAAGCTTCTT TGTGGCTTAC ACTGGAAATT ATGAAAGCAG	2100
	TTTTCTCCT AAGACTTTTG GTTCTCGCA TTGCCTCTCA GACTAAGCAC TAAAAAGCAA	2160
	AGCAAAACAG AACTAGTNCCT GTCTTAATGA AATATATCAA CCCAAAAGTG TAATGAGGAA	2220
45	AATGCTTCAT TAGTTTCCCC TAGCAGACTT TTACTTCTCT TACTGCTA CACCATTACT	2280
	TTCTTGAGAC ATTTGTAAGT CCTTGATAC AGAAGAGTGA TATTTAGGAG GNCITTAATG	2340
50	AAGGG	2345

55 (2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

5	TTTTTTTTTT TTTTTTTTTT TTTTNCNCAAG ATCATGTGTTT ATTTATTACT TCAGATAAAA	60
	AGATAGTATA CATATTAGGG AATCCCTTAA AATTCAACTC TAGAGTTATA CACCATCTAG	120
	TACTTTTGCA ATGAATGTTA ACAACAACAA AAAAAATCTC TAAACACCTG AAAGCCCCAC	180
10	TATTAACATG GACTATGGTA ATAAAAATT TTGACATTTA ATTTGTTCAT CATATAGTAT	240
	TTACATTATG AAACCAATGG TGATGATACA ATAAAGTGAT AAAGAAATAG TAAAAATAAA	300
15	CTTTAAAAAG CAAAGGTTTA TAGTCTGACA ATGCTAATTA TCCTAATGT ATATAAAAAA	360
	TTAAACATA GAGCTTTCTG TTACAAAATT CTTAATCCTC TGGGTGTGTA TCATTACTTG	420
	CTACCAATTT ACATGCAACA TCTGCTAGGA CTGACATTTG ATTTTTTTCC CCAAGAATGT	480
20	GTGAGTAGAT AAATGACATT TCAGAGCAGA TATTAATTTA CTTGTGGACA GAAAAAGAAA	540
	CTCAAGATTG GTACTGGTCA CAAGCCTCTT CCCAATAGAA ATTATAAAAA CAGTAAGATA	600
25	AAATTTAAAA AAAATCTAAA AAGGGGATGC ATAGGCAAAG AGTACCATAA ATGGCACAGC	660
	TCAAAAAATC CCAGGACCAA TCAGACACAC ATCTTTTCTC TCTCCTTCAG CGACAAGAGG	720
	TGGATTTTGC CATCAAATAA CCATGATTGA AGCAAGCGAG GGGCACCAGG TGTACAACTG	780
30	ATTAGATCTT GCAAATACT AAGATGGGAG CAGGGGTGGC CAGAAGAAGG GGTAATTTAT	840
	ATATAATTCA AACTATATAC AGCATAAATG GAATGCAGCC CATCCCAAAC TGGCTCTGTG	900
35	AAACAATTGG ACCTTTATAG TTAAAAATTAT AACAAGTGTA ATAATACAAT AGATTTACAT	960
	GGGAAGCAAA ATCCAAGGGA CATTTTATAT TAAGTATTTA CTGTGCTGTT TCAATTTAAA	1020
	AATAATTTTG CTAAGTATAC ATCTCAACTG AAGTCTATGT AAAAAATGTC CTAATAGATA	1080
40	CAGATATTTA CCTTTGGTGA GTTGAAGGCC TTTTGTGAC TTCTGTCTGA ACTGTAGGCA	1140
	GAATGCTAGA TGTACATGCA CATATGGAGA AACTCAAGCT GAGGTCATCC AAAAGCTGTG	1200
45	CGTATGAGGA GGCTGGAGGT ACTTTGAAAG TCAAAGTAGA CCAGAAACCC AAAACAGGTA	1260
	ACAGTGAGGA TGGCAACAGG GAATGGAATG CCAATATGGC AGTAAACTT TTTTAAAAA	1320
	CAGAAAGAGG AAGGCCTCTC GTACCAGCAG AATCCTGTAC ACGTACAAAA AAGAAAAAGC	1380
50	CACCCACCAT TTTGTAAAAC AGAAGCCAAT TATAGTGTGG GAAAGTACAA ATTACAGAAA	1440
	ACCAGAAGTC AACAGAAGAA AACTACTGG TTTACTTGAG AGAAAGGAGA ATGGTTCACC	1500
55	CCGAGCAGAG TTAATTGGTG AACGCCCA CCACGCCCA CAGAACCTCA TTGGTGTGG	1560
	CCTTCAGACA TTCCACTTCA GGTCTAAGT CGAGAARNTG CCGCACTCTC TTGGTAGCCA	1620
60	AATCATACTG CTCGTCCAGA AGAGGAGCAA AAGCATTCTC CAGGACGTCC GAGGCATGAG	1680



	CCAGGTAAAT GAGGGCCAGC AAGCGCCTGT CCATGCGGTG AGGGTCATTTC ACCCATTTGT	1740
	CAAGAACGGC TTCCTGTACT TTCTTGATGA GCGCGTGCTT AATGTTGTTA TTGGTGAGGG	1800
5	GATGTGTGT CATGTCAAAA AGTAGGAAGT TCTGTTTCTC TGTGTCAAT ACACCCTTTT	1860
	CCACCAGGTT TTTAGCTAAT CGTTCCTGTA CATTTCTTAA CTGATAATGC AATTTTAATG	1920
	GATTCATGT CTCACCACTA AGTAATTCAA TCCAGTTCTG GACCGTTTCT GGAGGCTGAG	1980
10	TTTCTTAAC ATGCTTCAGA GCTTCATCAA GAAGAACATC CCCTGTTGGA GCATCTGACT	2040
	TACAGATTAC CTTTCTTGTT AATAGACTTT TACGTCTCAT TCCACAAGCC TCTAGTTGTA	2100
15	ACCTTCCTCT CAATGCTAAT TCAATTAACTA TACAGCCACG TAATCCAGAT GATATACAGT	2160
	CATTCACAAA TGATGTGTAA ACCTTGCGGG TCCTTGAGGC CCAGCAGGAG CACTTCCTCC	2220
	ATCAGGGTCA GCCGCGTTTC CTTGGAGTCG CCCTTGTCGT CGTCGTCTG CTCGTGCGG	2280
20	CGGCTCTGCG CGTCGTCTTC GCTGCTAGCC GCGCGCGCGC CCGCCGCCCG CTCCTTGTG	2340
	GCGCGGTTGC GGGAGGCCTC GGTGCGCGG	2369

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(2) INFORMATION FOR SEQ ID NO: 303:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1181 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

	GGGACGTGTG GTTTCAGCTC GTGCGCCTCC CCGTGGGTTT GCGACGTTTA GCGACTATTG	60
40	CGCCTGCGCC ACGCCGGCTG CGAGACTGGG GCGGTGGYTG CTGGTCCCGG GTGATGCTAG	120
	GCGGCTCCCT GGGCTCCAGG CTGTTGCGGG GTGTAGGTGG GAGTCACGA CGGTTCGGGG	180
	CCCAGGTTGT CCGCGAAGGT GGCGCACATG GGCGGCAGG GAGAGCATGG CTCAGCGGAT	240
45	GGTCTGGGTG GACCTGGAGA TGACAGGATT GGACATTGAG AAGGACCAGA TTATTGAGAT	300
	GGCCTGTCTG ATAAGTACT CTGATCTCAA CATTTTGGCT GAAGGTCTTA ACCTGATTAT	360
50	AAAACAACCA GATGAGTTGC TGGACAGCAT GTCAGATTGG TGTAAGGAGC ATCACGGGAA	420
	GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG TACAATTACA TTGCAGCAGG CAGAGTATGA	480
	ATTTCTGTCC TTTGTACGAC AGCAGACTCC TCCAGGGCTC TGTCCTACTG CAGGAAATTC	540
55	AGTTTCATGA GATAAGAAGT TTCTTGACAA ATACATGCCC CAGTTCATGA AACATCTTCA	600
	TTATAGAATA ATTGATGTGA GCACTGTATA AGAACTGTGC AGACGCTGGT ATCCAGAAGA	660
60	ATATGAATTT GCACCAAAGA AGGCTGCTTC TCATAGGGCA CTTGATGACA TTAGTGAAAG	720

CATCAAAGAG CTTCACTTTT ACCGAAATAA CATCTTCAAG AAAAAAATAG ATGAAAAGAA 780  
 GAGGAAAATT ATAGAAAATG GGGAAAATGA GAAGACCGTG AGTTGATGCC AGTTATCATG 840  
 5 CTGCCACTAC ATCGTTATCT GGAGGCAACT TCTGGTGGTT TTTTTCCTC ACGCTGATGG 900  
 CTTGGCAGAG CMCTTCGGTT AACTTGCATC TCCAGATTGA TFACTCAAGC AGACAGCACA 960  
 10 CGAAATACTA TTTTCTCCT AATATGCTGT TTCCATTATG ACACAGCAGC TCCTTTGTAA 1020  
 GTACCAGGTC ATGTCCATCC CTGGTACAT ATATGCATTT GCTTTTAAAC CATTTCTTTT 1080  
 GTTTAAATAA ATAAATAAGT AAATAAGCT AGTTCTATTG AAATGCAAAA AAAAAAAAAA 1140  
 15 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA N 1181

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(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

30

CTTTTTGTTG TCCGGCCGAT CCCACCTCTC CTCGACCCCTG GACGTCTACC TTCCGGAGGC 60  
 CCACATCTTG CCCACTCCGC GCGCGGGGCT AGCGCGGGTT TCAGCGACCG GAGCCCTCAA 120  
 35 GGGACATGGC AACTACAGCG GCGCCGGCGG GCGCGGCCCG AANATGGAGC TGGCCCGGAA 180  
 TGGGGAGGGT TCGAAGAAAA CATCCAGGGC GGAGGCTCAG CTGTGATTGA CATGGAGAAC 240  
 ATGGATGATA CCTCAGGCTC TAGCTTCGAG GATATGGGTG AGCTGCATCA GCGCCTGCGC 300  
 40 GAGGAAGAAG TAGACGCTGA TGCAGCTGAT GCAGCTGCTG CTGAAGAGGA GGATGGAGAG 360  
 TTCTTGGCA TGAAGGGCTT TAAGGGACAG CTGAGCCGGC AGGTGGCAGA TCAGATGTGG 420  
 45 CAGGCTGGGA AAAGACAAGC CTCAGGGCC TTCAGCTTGT ACGCCAACAT CGACATCCTC 480  
 AGACCCTACT TTGATGTGGA GCCTGCTCAG GTGCGAACAG GGCTCCTGGA GTCCATGATC 540  
 CCTATCAAGA TGGTCAACTT CCCCCAGAAA ATTGCAGGTG AACTCTATGG ACCTCTCATG 600  
 50 CTGGTCTTCA CTCTGGTTGC TATCCTACTC CATGGGATGA AGACGTCTGA -CACTATTATC 660  
 CGGGAGGGCA CCCTGATGGG CACAGCCATT GGCACCTGCT TCGGCTACTG GCTGGGAGTC 720  
 55 TCATCCTTCA TTTACTTCCT TGCCCTACCTG TGCAACGCCC AGATCACCAT GCTGCAGATG 780  
 TTGGCACTGC TGGGCTATGG CCTCTTTGGG CATTGCATTG TCCTGTTCAT CACCTATAAT 840  
 60 ATCCACCTCC ACGCCCTCTT CTACCTCTTC TGGCTGTGG TGGGTGGACT GTCCACACTG 900

CGCATGGTAG CAGTGTGGT GTCTCGGACC GTGGGCCCCA CACAGCGGCT GTCCTCTGT 960  
 GGCACCTGG CTGCCCTACA CATGCTCTTC CTGCTCTATC TGCATTTTGC CTACCACAAA 1020  
 5 GTGNTAGAGG GGATCCTGGA CACACTGGAG GGCCCCAACA TCCCGCCCAT CCAGAGGGTC 1080  
 CCCAGAGACA TCCCTGCCAT GTCCTCTGCT GTCGGGCTTC CCACCACGCT CCTCAACGCC 1140  
 ACAGCCAAAG CTGTTGGGT GACCTGCGAG TCACACTGAC CCCACCTGAA ATTCTTGGCC 1200  
 10 AGTCCTCTTT CCCGCAGCTG CAGAGAGGAG GAAGACTATT AAAGGACAGT CCTGATGACA 1260  
 TGTTCGTAG ATGGGGTTG CAGCTGCCAC TGAGCTGTAG CTGCGTAAGT ACCTCCTTGN 1320  
 15 AGCTGTCGGC ACTTCTGAAA GCACAAGGCC AAGAACTCCT GGCCAGGACT GCAAGGCTCT 1380  
 GCAGCCAATG CAGAAAATGG GTCAGCTCCT TTGAGAAGCC CTCCCCACCT ACCCCTTCCT 1440  
 TCCTCTTTAT CTCTCCACA TTGTCTTGCT AAATATAGAC TTGTAATTA AAAAAAAAAA 1500  
 20 AAAAAAAAAA AAAAAAAAAA AAAAAAGGGG GGNCCCC 1537

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(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1493 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

35

TGCATGCCAA AACCAATGCC TGCCAAACAA AATCTTAGAC ATCCCAATAT AATATGTTAG 60  
 TTATATTTCT ATTCACATCA TTATIGAAAA TACCCAGCTC AGTGCCTGGC TTAATAAATG 120  
 40 TTAAATTCCT TTACCTACTC TTGCTCTATT TTTTATTG AAATGGAGAT GAGCAAATA 180  
 ACACATTCAT GGCTGAAGCA ATTTTGTGGA CATTTCTGT TACCAAAAGA TCTATAATCA 240  
 GGATGATCCT GAGCTGTICA AACAGCTGT ATATAAACAG ACAATGAAAC TCTTGCAGA 300  
 45 GCTGGAAATT AAAAGGAAAG AGAGAGAAGC CAAAGAGATG CATGAAAGGA AACGACAAAG 360  
 GGAAGAAGAG ATTGAAGCTC AAGAAAAAGC CAAACGGGAA AGAGAGTGGC AGAAAACTT 420  
 50 TGAGGAAAGT CGAGATGGTC GTGTGGACAG CTGGCGAAAC TTCCAAGCCA ATACGAAGGG 480  
 GAAGAAAGAG AAGAAAAATC GGACCTTCCT GAGACCACCG AAAGTAAAAA TGGAGCAACG 540  
 TGAGTGACCG CCCAAGGTCA CAGGCACAGA ACCTTTCCCC TGCTATCTCC CTTCCTGCTT 600  
 55 CGAAGGACTC ATTCTTTCCT CCCACTTCCA CCCCAACATA GAGTAGTATT TGCTTTTGTAG 660  
 TCCATTTTGT TTTCAATACG ATTTAATATC GATCAGAGTA ATTCTTTTGT ACATTGAAAT 720  
 60 GAGGGGCTTG GTTTAAAAAA AGACCTTTCC CTCTCCCTGC CCCTAGAACA ACCAGTATTA 780

GAAGGTGCCA CCATGGTGC TGCTTCTCT TCCACAGCC TGTAATCAG TGTTTGTAC 840  
 5 TTCACTGAAT TGTGATGGT AGAACTTCG TGGATAGTT GTGAAATCA TCCAATTAAA 900  
 CATACTGCTT AAAACAGTG TGCTGTGACT TCAGAGACAA GCCTGGAAGG GGCACCTTAG 960  
 GAAGCCCTT CGCTTCAGT GCTCGCTTCT GGGTGTGCTC CCTTGAAGG CCCAGATAAG 1020  
 10 ACAGGAACA CTTGTGAGCA CACAGAGCAG CATCTGATGC CCTGTGGTGT TTGGCATGTG 1080  
 CCCCCTGTCT ACTGACCAAT CAGTGTGGCA TGAGGCCAC GCCACCCAA CTTTCACTT 1140  
 TCCAAGAGC TAGCCGTCT CACCCAGTA CCAATGCTTA GCCTGTCTGC ATTTGTTAGT 1200  
 15 GGTAAATATC TTTATGTATA ATAAATTTT ATACCCAAGC CATTGATGTA CTTTCTCTG 1260  
 TACTCTCCCT TGTGGGTCCC TTGTCTGGCT TGGCTGAACC CAAAATGCT TTGGGGTTGG 1320  
 20 ACAGACCTGG CTGAACCTTA GTTCTTTCAT CTATGAAATG GGAATATGAA TTACTGCAGC 1380  
 AGCTTTTAGG GCAGATTTC CATGGCATAT ACAAGGTAAC TACCATAGTG CTCCTTGGGT 1440  
 25 ATTGCCAATA TCCTATTATT TCTGTGTAAA ATGAAGATAC TGATTGTTTT GAG 1493

30 (2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

40 AATTCGGCAG AGGNATTATA TACACTATAC TGGCATTAC TGTTTCACCC AGCCCGGAAA 60  
 GTCAGAGATG TATATTGGAA AATTTACAAC TCCATCTACA TTGGTTCCCA GGACGCTCTC 120  
 ATAGCACATT ACCCAAGAAT CTACAAGAT GATAAGAACA CCTATATTCG TTATGAACTT 180  
 45 GACTATATCT TATAATTTTA TTGTTTATTT TGTGTTTAAT GCACAGCTAC TTCACACCTT 240  
 AAACTTGCTT TGATTGGTG ATGTAACTT TTAACATG CAGATCAGTG TAGAACTGGT 300  
 CATAGAGGAA GAGCTAGAAA TCCAGTAGCA TGATTTTAA ATAACCTGTC TTGTTTGTG 360  
 50 ATGTTAAACA GTAAATGCCA GTAGTGACCA AGAACACAGT GATTATATAC ACTATACTGG 420  
 AGGGATTCA TTTTAAATC ATCTTTATGA AGATTAGAA CTCATTCCTT GTGTTTAAAG 480  
 55 GGAATGTTTA ATTGAGAAAT AAACATTTGT GWACAAAATG YTAACAAAAA AAAAAAAAAA 540  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACTCGA 577

60

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2860 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GTGTNGACCG CTCTCNCAAT ATGGCTCCCC CGGGCTGGCA GRWRKTCRGT CWCKRGTGGC 60  
 TAGCCTGTCC TGACAGGGGA GAGTTAAGCT CCCGTTCTCC ACCGTGCCGG CTGGCCAGGT 120  
 15 GGGCTGAGGG TGACCGAGAG ACCAGAACT GCTTGCTGGA GCTTAGTGCT CAGAGCTGGG 180  
 GAGGGAGGTT CGCCGCTCC TCTGCTGTCA GCGCCGGCAG CCCCTCCCGG CTTCACCTTC 240  
 20 TCCCCGAGCC CTGCTACTG AGAAGCTCCG GGATCCCAGC AGCCGCCACG CCCTGGCCTC 300  
 AGCCTGCGGG GCTTCCAGTC AGGCCAACAC CGACGCGCAC TGGGGAGGAA GACAGGACCC 360  
 TTGACATCTC CATCTGCACA GAGGTCCTGG CTGGAACCGA GCAGCCTCCT CCTCCTAGGA 420  
 25 TGACCTCACC CTCCAGCTCT CCAGTTTTC A GGTGGAGAC ATTAGATGGA GGCCAAGAAG 480  
 ATGGCTCTGA GCGGACAGA GGAAAGCTGG ATTTTGGGAG CGGGCTGCCT CCCATGGAGT 540  
 30 CACAGTTCCA GGGGAGGAC CGGAAATTCG CCCCTTCAGA TAAGAGTCAA CCTCCAACTA 600  
 CCGAAAGGGA ACAGGTGCCA GTCAGCCGGA TCCAAACCGA TTTGACGAG ATCGGCTCTT 660  
 CAATGCGGTC TCCCGGGGTG TCCCGGAGGA TCTGGCTGGA CTTCAGAGT ACCTGAGCAA 720  
 35 GACCAGCAAG TACCTCACCG ACTTCGGAAA TACACAGAGG GCTCCACAGG TAAGACGGCC 780  
 TGATGAAGGC TGIGCTGAAA CCTTAAGGAC GGGGTCAATG CCTGCATTCT GCCACTGCTG 840  
 40 CAGATCGACC GGGACTCTGG CAATCTCAG CCCCTGGTAA ATGCCAGTG CACAGATGAC 900  
 TATTACCGAG GCCACAGCGC TCTGCACATC GCCATTGAGA AAGAGGAGTC TGCAGTGTGT 960  
 GAAGCTCCTG GTGGAGAATG GGGCCAATGT GCATGCCCGG GTCTGCGGCG ACTTCTTCCA 1020  
 45 GAAGGGCCAA GGGACTTGCT TTTATTTTCG TGAGCTACCC CTCTCTTTGG CCGCTTGCAC 1080  
 CAAGCAGTGG GATGTGGTAA GCTACCTCCT GGAGAAACCA CACCAGCCCG CCAGCCTGCA 1140  
 50 GGCCACTGAC TCCAGGGCA ACACAGTCCT GCATGCCCTA GTGGATGATC TCGGACAACT 1200  
 CAGCTGAGAA CATTGCACTG GTGACCAGCA TGTATGATGG GCTCCTCAA GCTKGGGSCC 1260  
 SCCYTCTGCC CTACCGTGCA GCTTGAGGAC ATCCGCAACC TGCAGGATCT CACGCCTCTG 1320  
 55 AAGCTGGCCG CCAAGGAGGG CAAGATCGAG ATTTTCAGGC ACATCCTGCA GCGGGAGTTT 1380  
 TCAGGACTGA GCCACCTTTC CCGAAAGTTC ACCGAGTGGT GCTATGGGCC TGTCCGGGTG 1440  
 60 TCGCTGTATG ACCTGGCTTC TGTGGACAGC TGTGAGGAGA ACTCAGTGCT GGAGATCATT 1500

	GCCTTTCATT GCAAGAGCCC GCACCGACAC CGAATGGTCG TTTTGGAGCC CCTGAACAAA	1560
5	CTGCTGCAGG CGAAATGGGA TCTGCTCATC CCCAAGTTCT TCTTAACTT CCTGTGTAAT	1620
	CTGATCTACA TGTTCATCTT CACCGCTGTT GCCTACCATC AGCCTACCCT GAAGAAGCAG	1680
	GCCGCCCCCTC ACCTGAAAGC GGAGGTGGGA AACTCCATGC TGCTGACGGG CCACATCCTT	1740
10	ATCCTGCTAG GGGGGATCTA CCTCCTCGTG GGGCCAGCTG TGGTACTTCT GGCGGCGCCA	1800
	CGTGTTCATC TGGATCTCGT TCATAGACAG CTACTTTGGA AATCCTCTTC CTGTTCCAGG	1860
	CCCTGCTTCA CAGTGGTGTG CCAGGTGCTG TGTTCCTGCG GCCATCGAGT GGTACCTGCC	1920
15	CCTGCTTGTC TCTGCGCTGG TGGCTGGGCT GGCTGAACCT GCTTTACTAA TACACGTGGC	1980
	GTTCCAGCAC ACAGGCAGTC TACAGTTTCA TGWTCCCTGA AGCCCTGGTG AGCCTGAGCC	2040
20	AGGAGGCTTG GCGCCCCGAA GTCCTACAG GCCCAATGC CACAGAGTCA GTGCAGCCCA	2100
	TGGAGGGACA GGAGGACGAG GGCAACGGGG CCCAGTACAG GGGTATCCTG GAAGCCTCCT	2160
	TGGAGCTCTT CAAATTCACC ATCGGCATGG GCGAGCTGGC CTCCAGGAG CAGCTGCACT	2220
25	TCCGCGGCAT GGTGCTGCTG CTGCTGCTGG CCTACGTGCT GCTCACCTAC ATCCTGCTGC	2280
	TCAACATGCT CATCGCCCTC ATGAAGCGAA CGTCACAGTG TCCCACTGA CAGCTGGAGC	2340
30	ATCTGGAAGC TGCAGAAAGC CATCTCTGTC CTGGAGATGG AGAATGGCTA TTGGTGGTGC	2400
	AGGAAAAAGC AGCGGGCAGG TGTGATGCTG ACCGTGGGCA CTAAGCCAG ATGGCAGCCC	2460
	CGATGAGCGC TGGTGCTTCA GGGTGGAGGA GGTGAACTGG GCTTCATGGG GAGCAGACGC	2520
35	TGCCTACGCT GTGTGAGGAC CCGTCAGGGG CAGGTGTCCC TCGAACTCTC GAGAACCCTG	2580
	TCCTGGCTTC CCTCCCAAG GAGGATGAGG ATGGTGCTC TGAGGAAAAC TATGTGCCCG	2640
40	TCCAGCTCCT CCAGTCCAAC TGATGGCCCA GATGCAGCAG GAGGCCAGAG GACAGAGCAG	2700
	AGGATCTTTC CAACCACATC TGCTGGCTCT GGGGTCCCAG TGAATTCTGG TGGCAAATAT	2760
45	ATATTTTCAC TAACTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAVGAGGG GGGGCCCGKT	2820
	ASCCAAWTTC GCCCTATAAG TGAGTGCCWA TTACGATAAA	2860

50

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

	CTGCTTGTGT CTGCGCTGGT GCTGGGCTGG CTGAACCTGC TTTACTATAC ACGTGGCTTC	60
	CAGCACACAG GCATCTACAG TGTCTATGATC CAGAAGCCCT GGTGAGCCTG AGCCAGGANN	120
5	TTGGCGCCCC GAAGCTCCTA CAGGCCCAA TGCCACAGAG TCAGTGCAGC CCATGGAGGG	180
	ACAGGAGGAC GAGGGCAACG GGGCCAGTA CAGGGGTATC CTGGAAGCCT CTTTGGAGCT	240
10	CTTCAAATTC ACCATCGGCA TGGGCGAGCT GGCTTCCAG GAGCAGCTGC ACTTCCGGG	300
	CATGGTGCTG CTGCTGCTGC TGGCTACGT GCTGCTCACC TACATCCTGC TGCTCAACAT	360
	GCTCATCGCC CTCATGNAGC GAGACCGWCA ACAGTGTCCG CACTGACAGC TGGAGCATCT	420
15	GGAGAGTGA GAAAGCCATC TCTGTCTGG AGATGGAGAA TGGCTATTGG TGGTGCAGGA	480
	AGAAGCAGCG GGCAGGTGTG ATGCTGACCG TTGGCACTAA GCCAGATGCG AGCCCCGATG	540
20	AGCGCTGGTG CTTGAGGTG GAGGAGGTGA ACTGGGCTTC ATGGGAGCAG ACGCTGCCTA	600
	CGCTGTGTGA GGACCCGTC GGGGAGGTG TCCCTCGAAC TCTCGAGAAC CCTGTCTGG	660
	CTTCCCTCC CAAGGAGGAT GAGGATGGT CTTCTGAGGA AAATATGTG CCCGTCCAGC	720
25	TCTCCAGTC CAACTGATGG CCCAGATGCA GCAGGAGGCC AGAGGACAGA GCAGGAGATC	780
	TTTCCAACCA CATCTGCTGG CTCTGGGGTC CCACTGAATT CTGGTGGCAA ATATATATTT	840
30	TCACTAAMMM AAAAAAAAAA AAAAAAAAAA ACTCGA	876

## (2) INFORMATION FOR SEQ ID NO: 309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2025 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

45	CATGACCCGC CTGATGCGAT CCCGCACAGC CTCTGGTTCC AGCGTCACTT CTCTGGATGG	60
	CACCCGCAGC CGCTCCCA CAAGCGAGGG CACCCGAAGC CGCTCCCA CAAGCGAGGG	120
	CACCCGCAGC CGCTGCACA CCAGCGAGGG GGCCACCTG GACATCACCC CCAACTCGGG	180
50	TGCTGCTGGG AACAGCGCGG GCCCAAGTCC ATGGAGGTCT CCTGCTAGGC GGCTGCCCA	240
	GCTGCCGCCC CCGACTCTG ATCTCTGTAG TGGCCCCCTC CTCCCGGCC CCTTTTGGCC	300
55	CCCTGCCTGC CATACTGCG CTAAGTGGT ATTAATCCAA AGCTTATTTT GTAAGAGTGA	360
	GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC TCTCCAAAG CGGGGTGGCG	420
	GTGGACCAA GGAAGGAAGC AAGCATCTCC GCATCGCATC CTCTTCCATT AACCAGTGGC	480
60	CGGTTGCCAC TCTCTCCCC TCCCTCAGAG ACACCAAAC GCAAAAACA AGACCGGTAC	540

	AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCTGAGC ATCCTGGTTC AAACGGGTGC	600
5	CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTTCCTCTTT AACTGAGGAG AAGCTGATCC	660
	AGTTTCCGGA AACAAAATCC TTTTCTCATT TGGGGAGGGG GGTAATAGTG ACATGCAGGC	720
	ACCTCTTTTA AACAGGCAAA ACAGGAAGGG GGAAAAGTG GGATTCATGT CGAGGCTAGA	780
10	GGCATTGGA ACAACAAATC TACGTAGTTA ACTTGAAGAA ACCGATTTT AAAGTTGGTG	840
	CATCTAGAAA GCTTTGAATG CAGAAGCAAA CAAGCTTGAT TTTTCTAGCA TCCTCTTAAT	900
15	GTGCAGCAAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG AAAAAATAT TTCAGCAAA	960
	GTTGGGCATC ATGGTTTGTG AAGGCTTAG TTCTGCTTTC TGCCTCTCCT CCACAGCCCC	1020
	AACCTCCAC CCCTGATACA TGAGCCAGTG ATTATTCTTG TTCAGGGAGA AGATCATTTA	1080
20	GATTTGTTTT GCATTCCTTA GAATGGAGGG CAACATTCCA CAGCTGCCCT GGCTGTGATG	1140
	AGTGTCTTG CAGGGCCCG AGTAGGAGCA CTGGGGTGGG GCGGAATTG GGGTTACTCG	1200
25	ATGTAAGGA TTCTTGTTG TTGTGTGAG ATCCAGTGA GTTGTGATTT CTGTGGATCC	1260
	CAGCTTGGTT CCAGGAATTT TGTGTGATTG GCTTAAATCC AGTTTTCAT CTTCGACAGC	1320
	TGGGCTGGAA CGTGAAGTCA GTAGCTGAAC CTGTCTGACC CGGTACGTT CTGGATCCT	1380
30	CAGAACTCTT TGCTCTGTC GGGGTGGGG TGGGAAGTCA CGTGGGAGC GGTGGCTGAG	1440
	AAAATGTAAG GATTCCTGAA TACATATTCC ATGGGACTTT CCTTCCCTCT CTGCTTCCT	1500
35	CTTTTCTGCT TCCCTAACCT TTCGCCGAAT GGGGCAGCAC CACTGACGTT TCTGGGCGGC	1560
	CAGTGGGCT GCCAGGTTC TGTACTACTG CCTGTACTT TTCATTTTGG CTCACCGTGG	1620
	ATTTTCTCAT AGGAAGTTTG GTCAGAGTGA ATTGAATATT GTAAGTCAGC CACTGGGACC	1680
40	CGAGGATTTT TGGGACCCCG CAGTTGGGAG GAGGAAGTAG TCCAGCCTTC CAGGTGGCGT	1740
	GAGAGGCAAT GACTCGTTAC CTGCCGCCA TCACCTTGA GGCCTTCCCT GGCCTTGAGT	1800
45	AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGAGTACGA TGGGAACTA TTGTGCACAA	1860
	GTCTTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA TTTCCAGACC AATAAATTTG	1920
	TAACTTTGCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAACTC	1980
50	GAGGGGGGCC CGTACCCAAT TCGCCGTATA TGATCGTAAA CAATC	2025

55 (2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3026 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

5	TAGGCAGCAC TGAAATATCC TAACCCCTA AGCTCCAGGT GCCCTGTGGN ACGAGCAACT	60
	GGACTATAGC AGGGCTGGGC TCTGTCTTCC TGGTCATAGG CTCACTCTTT CCCCCAAATC	120
	TTCTCTGGA GCTTTGCAGC CAAGGTGCTA AAAGGAATAG GTAGGAGACC TCTTCTATCT	180
10	AATCCTTAAA AGCATAATGT TGAACATTCA TTCAACAGCT GATGCCCTAT AACCCCTGCC	240
	TGGATTCTT CCTATTAGGC TATAAGAGT AGCAAGATCT TTACATAATT CAGAGTGGTT	300
15	TCATTGCCTT CCTACCTCT CTAAATGGCC CTCCATTTAT TTGACTAAAG CATCACACAG	360
	TGGCACTAGC ATTATACCAA GAGTATGAGA AATACAGTGC TTTATGGCTC TAACATTACT	420
	GCCTTCAGTA TCAAGGCTGC CTGGAGAAAG GATGGCAGCC TCAGGGCTTC CTTATGTCCT	480
20	CCACCACAAG AGCTCCTTGA TGAAGGTCAT CTTTTCCTCC TATCCTGTTT TCCCTCTCC	540
	CGCTCCTAAT GGTACGTGGG TACCCAGGCT GGTTCCTGGG CTAGGTAGTG GGGACCAAGT	600
25	TCATTACCTC CCTATCAGTT CTAGCATAGT AACTACGGT ACCAGTGTTA GTGGGAAGAG	660
	CTGGGTTTTC CTAGTATACC CACTGCATCC TACTCCTACC TGGTCAACCC GCTGCTTCCA	720
	GGTATGGGAC CTGCTAAGTG TGGAATTACC TGATAAGGGA GAGGAAATA CAAGGAGGGC	780
30	CTCTGGTGT CTGGCCTCA GCCAGCTGCC CACAAGCCAT AAACCAATAA AACAAGAATA	840
	CTGAGTCAGT TTTTATCTG GGTCTCTTC ATTCCTACTG CACTTGGTGC TGCTTTGGCT	900
35	GACTGGGAAC ACCCCATAAC TACAGAGTCT GACAGGAAGA CTGGAGACTG TCCACTTCTA	960
	GCTCGGAAGT TACTGTGTAA ATAACTTTC AGAACTGCTA CCATGAAGTG AAAATGCCAC	1020
	ATTTTGTCTT ATAATTCTA CCCATGTTGG GAAAACTGG CTTTTTCCCA GCCCTTCCA	1080
40	GGGCATAAAA CTCAACCCCT TCGATAGCAA GTCCCATCAG CCTATTATTT TTTTAAAGAA	1140
	AACCTGCACT TGTTCCTCT TTTACAGTTA CTCTCTCCT GCCCCAAAT TATAAACTCT	1200
45	AAGTGTA AAAAGTCTTA ACAACAGCTT CTGCTTGTA AAAATATGTA TTATACATCT	1260
	GTATTTTAA ATCTGCTCC TGAAAAATGA CTGTCCATT CTCCACTCAC TGCAATTGGG	1320
	GCCTTCCCA TTGGTCTGCA TGTCTTTTAT CATTCAGGC CAGTGGACAG AGGGAGAAGG	1380
50	GAGAACAGGG GTCGCCAACA CTTGTGTTGC TTTCTGACTG ATCCTGAACA AGAAAGAGTA	1440
	ACACTGAGGC GCTCGCTCCC ATGCACAACT CTCCAAAACA CTTATCCTCC TGCAAGAGTG	1500
55	GGCTTCCAG GGTCTTACT GGAAGCAGT TAAGCCCCCT CTCACCCCT TCCTTTTTTC	1560
	TTTCTTACT CTTTGGCTT CAAAGGATTT TGGAAAAGAA ACAATATGCT TTACTCAT	1620
60	TTTCAATTC TAAATTGCA GGGGATACTG AAAAATACGG CAGGTGGCCT AAGGCTGCTG	1680

	TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT TACAAGATAA AAAACGAATC CCCTAAACAA	1740
	AAAGAACAAT AGAACTGGTC TTCCATTTTG CCACCTTTCC TGTTCATGAC AGCTACTAAC	1800
5	CTGGAGACAG TAACATTTCA TTAACCAAAG AAAGTGGGTC ACCTGACCTC TGAAGAGCTG	1860
	AGTACTCAGG CCACTCCAAT CACCCTACAA GATGCCAAGG AGGTCCCAGG AAGTCCAGCT	1920
	CCTTAAACTG ACGCTAGNMA ATAAACCTGG GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT	1980
10	CCATCTGTGA GGTGAYAGG AAGGATGAAA GACAAAGAAG GAAAAGAGTA TCAAAGGCAG	2040
	AAAGGAGATC ATTTAGTTGG GTCTGAAAGG AAAAGTCTTT GCTATCCGAC ATGTACTGCT	2100
15	AGTACCTGTA AGCATTTTAG GTCCAGAAT GGAAAAAAA ATCAGCTATT GGTAAATATA	2160
	TAATGTCCTT TCCCTGGAGT CAGTTTTTTT AAAAAGTTAA CTCTTAGTTT TTA CTGTGTTT	2220
	AATTCTAAAA GAGAAGGGAG CTGAGGCCAT TCCCTGTAGG AGTAAAGATA AAAGGATAGG	2280
20	AAAAGATTCA AAGCTCTAAT AGAGTCACAG CTTTCCCAGG TATAAACCT AAAATTAAGA	2340
	AGTACAATAA GCAGAGGTGG AAAATGATCT AGTTCTTGAT AGCTACCCAC AGAGCAAGTG	2400
25	ATTTATAAAT TTGAAATCCA AACTACTTTC TTAATATCAC TTTGGTCTCC ATTTTTCCTCA	2460
	GGACAGGAAA TAGTCCCCC CTAACCTTTC TTGCTTCAAA AATTAAAAATC CAGCATCCCA	2520
	AGATCATTTCT ACAAGTAATT TTGCACAGAC ATCTCCTCAC CCCAGTGCCT GTCTGGAGCT	2580
30	CACCCAAGGT CANCCAACA ACTTGTTGT GAACCCAAT GCCTTAACCT TCTGGGGGAG	2640
	GGGGATTAGC TAGACTAGGA GACCCAGAAG TGAATGGGAA AGGGTGAGGA CTTCACAATG	2700
35	TTGGCCTGTC AGAGCTTGAT TAGAAGCCAA GACAGTGGCA GCAAAGGAAG ACTTGGCCCA	2760
	GGAAAAACCT GTGGGTTGTG CTAATTTCTG TCCAGAAAAT AGGGTGGACA GAAGCTTGTC	2820
	GGGTGCATGG AGGAATTGGG ACCTGGTTAT GTTGTTATTC TCGGACTGTG AATTTTGGTG	2880
40	ATGTAAACA GAATATTCTG TAAACCTAAT GTCTGTATAA ATAATGAGCG TTAACACAGT	2940
	AAAATATTCA ATAAGAAGTC AAAAAAAAAA AAAAAAACT CGAGGGGGGG CCCGGTACCC	3000
45	AATTTNCCAA ATAGAGATNG TATTAC	3026

50 (2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 712 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

60 GCAGGCTTTG TGCTCACCTA CAAGCTGGGT GAGCAGGTG CCAGCAGCCT GTTTCCTCTT 60

CTCTGCTGG ACCACGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG TGTGGGTGCT 120  
 GTGGTCTGCT CCATCGCTGG CTCCTCCCTG GGTGGGACCT TGCTGGCCAA GCACTGGAAA 180  
 5 CTGCTGCCTC TGTGARGTC GGTGCTGCGC TTCCGCTCG GGGCCTAGC CTGTCAGACT 240  
 GCCTTGGTCT TCCACCTGGA CACCCTGGGG GCCAGCATGG ACGCTGGCAC AATCTTGAGA 300  
 10 GGGTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GAGGCCTGGT CACCACAGTC 360  
 ACCTTCACTG GGATGATGCG CTGCAGCCAG CTGGCCCCCA GGGCCTGCAG GCCACACACT 420  
 ACAGCCTTCT GGCCACGCTG GAGCTGCTGG GGAAGCTGCT GCTGGGCACT CTGCGGAGGC 480  
 15 CTGGCTGATG GGTGGGGCC ACATCCCTGC TTCTTGCTCC TGCTCATCCT CTCTGCCTTT 540  
 CCCGTCTGT ACCTGGACCT AGCACCAGC ACCTTCTCT GAGCTGAGTG GCTGGAGTGG 600  
 20 TCAATAAAGC CACATGTGCC TGTGGCCCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 660  
 AACTGGAGGG GGGGCCCGGT ACCCAAATCG CCGGATATGA TCGTAAACAA TC 712

25

(2) INFORMATION FOR SEQ ID NO: 312:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1289 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CAAAATTTCA GAACTTTCAG GAGGGCAAGA GAATATCAAA CAAAGATTTC TGAAGTATT 60  
 TTGCCAACCT TCTGGTTGAG CTGCAAGAAA ATATTATGAG TGAGAACTTT TCTGTTTCCC 120  
 40 GTTATTGGGT TTTTGGTTGG TTTTGTGTTG TTTTGTACTA TGCTTTGGTC TGTAAAAATA 180  
 TGCAACTGAA CTACATTCAG AAGGAAATAT TGTCTACATA GAATATTATA TGAAGTTGGT 240  
 45 ACATAATTCT GATGAGGAAA AAAAATCTTT GCAATTCTTT AAGCCATATT GTTGTMTTTC 300  
 TGTGTGTTT TCCCTGGATG AAAATATCAG TATTAAGTAG ACAGCATATT ATTCAAGTGT 360  
 TTAGACTTAT TAATATGTTT TTGTCTGTA TTTATACATA TGTGTATTTT GGAAAGTATT 420  
 50 GCCTTTTTTA AGGGAAGCTA TAATTCGATA CATAGTGAAA AAGGGAATGG TGACCCCTTT 480  
 GTGCCTCTTC CACTGAGGAT AACAAACAGC ATTGTAATCC ATTCTCTTGC ACCTTCTTCT 540  
 55 TCTTATCTTG TTATTACGGT TTTATTAATT TTGTAGAGGG ACAGGGAGTG GGCAAGGGGA 600  
 AGAAGCAGCT TATTTGACTA ACCAGCCCCT CTGTGGTCCA CCAGCGTCTT GCCTTGGTGG 660  
 GAGGGCTCTC AATCAGCAGG GCCCCAGGAG GGAAGAAGAA GTGGGGCAAA GCCTGGCCTC 720  
 60

GCGGCTCGGG AGCTTTGCCA TCTGAGCCAC GCCTCCTCCA GGCCATGCTC CTTGAACTTG 780  
 GAAATGTCAA CCGGAGCCCT TACACCAGCC CTCCAGCATC TAATAGACTT GAATCTACTC 840  
 5 TAAACGAATA TTTAATCCAA CCTCACTACA TTGTAGCTCA GTCCAACGAC TAACCCTGAA 900  
 ATGGGGGTGT TCCAGCCTTC AGCGAGATGG CCAAGCGGTC CCCTGGGGGC TGTGGCAGCG 960  
 GGCTTATCCT TCTCTGTTC CAACCTTGCC GTCCGACCTC CTCCGCCCCC ATCGGGTGAC 1020  
 10 CCGTCCGTG TCTGTGTCTG TCCATACGTG TGAGTCCAGC TAAAAAGACA AAACAGAACC 1080  
 CGTGGGCCCA GCTCGGAAGG TCGTGGAGA AGGCTCCGAC GTCTCCGAAG TGCAGCCCTT 1140  
 15 GGGATGGCAT TCCGTTGTGT GCCTTATTCC TGGAGAATCT GTATACGGCT CGCCTATAGA 1200  
 AATATAGCCT CTTTCATGCTG TATTAAAAGG ACTTTTAAAA GCAAAAAAAA AAAAAAAA 1260  
 CTTGAGGGGG GGNCCGTAC CCAATTNTC 1289  
 20

25 (2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Ile Leu Phe Ser Ser Ser  
 1 5 10 15

35 Leu Pro Phe Leu Trp Leu  
 20

40 (2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Met Phe Leu Thr Gln Gly Gly Pro Leu Pro Ser Thr Arg Ala Arg  
 1 5 10 15

50 Pro Thr Cys Gln Ala Gly Ala Leu Pro Lys Pro Ser Gly Leu Leu Gly  
 20 25 30

55 Val Thr Cys Trp Asn Gly Leu Lys Gly Pro Leu Cys Gly Asn Arg Cys  
 35 40 45

Ser Pro Asn Thr Leu Leu Leu Ala Ala Arg Gln Ala Leu Trp Lys Gly  
 50 55 60

60 Arg Gly Arg Thr His Gln Asp Leu Pro Gly Pro Leu Gln Gly Arg Gln

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

25 Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu  
1 5 10 15  
Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser  
20 25  
30

(2) INFORMATION FOR SEQ ID NO: 316:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

40 Met Asp Gly Phe Ser Ser Arg Leu Phe Ser Ser Leu Pro Phe Val Ala  
1 5 10 15

45 Leu Gln Trp Phe Ile Val Ile Ser His Leu Leu Ser Leu Ser Leu Ser  
20 25 30

Ala Cys Cys Tyr Gln Thr His Cys Ser Leu Xaa Gln Leu Ser Ser Ala  
35 40 45

50 Phe Ser Xaa Met Gly Glu Ser Cys Val Gly Glu Arg Glu Tyr Xaa Phe  
50 55 60

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

5

Met Pro Leu Ile Asn Leu Leu Leu Leu Tyr Tyr Val Pro Asn Gly Gly  
 1 5 10 15

10

Lys Gln Asp Lys Lys  
 20

15

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Gly Arg His Leu Val Leu Val Met Phe Ile Thr Thr Ser Leu His  
 1 5 10 15

25

Ser Gly Thr Pro Val Pro Glu Asn Val Ile Cys Gly Val Thr Lys Gly  
 20 25 30

Pro Gln Gly Lys Lys Lys Lys  
 35

30

(2) INFORMATION FOR SEQ ID NO: 319:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Leu Trp Trp Ser Arg Asp Tyr Thr Met Val Phe Leu Leu Phe Thr  
 1 5 10 15

45

Met Val Phe Thr Gly Asp Leu Val Ile Arg Gly Arg Thr Glu Leu Ser  
 20 25 30

Leu

50

(2) INFORMATION FOR SEQ ID NO: 320:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

60

Met Val Cys Ser Ser Leu Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe

1                    5                    10                    15  
 Ile Val Phe Arg Leu Arg Glu Val Trp Gln Ala Leu Pro Leu Ile Leu  
                   20                    25                    30  
 5 Phe Ala Val Leu Gly Leu Leu Ala Ala Gly Val Thr Leu Leu Leu Pro  
                   35                    40                    45  
 10 Glu Thr Lys Gly Val Ala Leu Pro Glu Thr Met Lys Asp Ala Glu Asn  
                   50                    55                    60  
 Leu Gly Arg Lys Ala Lys Pro Lys Glu Asn Thr Ile Tyr Leu Lys Val  
                   65                    70                    75                    80  
 15 Gln Thr Ser Glu Pro Ser Gly Thr  
                   85

20 (2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Gln Pro Gly Ala Gly Val Leu Val Leu Gly Leu Leu Leu Pro Pro  
                   1                    5                    10                    15  
 30 Pro Gln Ser Pro Ser Leu Ser  
                   20

35

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Thr Phe Thr Leu Gly Asp Ser Gln Val Leu Leu Ile Asn Leu Phe  
                   1                    5                    10                    15  
 45 Pro Ser Met Pro Ser Gly Ser Cys Ala Arg Pro  
                   20                    25

50

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

60 Met Cys Leu Glu Cys Trp Ala Glu Asn Leu Gly Pro His His Thr Ser

	1			5					10				15			
	Ser	Leu	Leu	Asn	Pro	Arg	His	Leu	Pro	Ser	Ile	Pro	Ala	Met	Phe	Pro
				20					25					30		
5	Val	Ser	Ser	Gly	Cys	Phe	Gln	Glu	Gln	Glu	Met	Asn	Lys	Ser	Leu	
				35				40					45			
	Val	Ser	Cys	Leu	Phe	Val	Leu	His	Phe	Val	Leu	His	Cys	Ile	Phe	Xaa
10			50				55					60				

15

(2) INFORMATION FOR SEQ ID NO: 324:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

25	Met Leu Ser Thr Ser Glu Tyr Ser Gln Ser Pro Lys Met Glu Ser Leu
	1                      5                      10                      15
	Ser Ser His Arg Ile Asp Glu Asp Gly Glu Asn Thr Gln Ile Glu Asp
	20                      25                      30
30	Thr Glu Pro Met Ser Pro Val Leu Asn Ser Lys Phe Val Pro Ala Glu
	35                      40                      45
	Asn Asp Ser Ile Leu Met Asn Pro Ala Gln Asp Gly Glu Val Gln Leu
35	50                      55                      60
	Ser Gln Asn Asp Asp Lys Thr Lys Gly Asp Asp Thr Asp Thr Arg Asp
	65                      70                      75                      80
40	Asp Ile Ser Ile Leu Ala Thr Gly Cys Lys Gly Arg Glu Glu Thr Val
	85                      90                      95
	Ala Glu Glu Val Cys Ile Asp Leu Thr Cys Asp Ser Gly Ser Gln Ala
	100                      105                      110
45	Val Pro Ser Pro Ala Thr Arg Ser Glu Ala Leu Ser Ser Val Leu Asp
	115                      120                      125
	Gln Glu Glu Ala Met Glu Ile Lys Glu His His Pro Glu Glu Gly Ser
50	130                      135                      140
	Ser Gly Ser Glu Val Glu Glu Ile Pro Glu Thr Pro Cys Glu Ser Gln
	145                      150                      155                      160
55	Gly Glu Glu Leu Lys Glu Glu Asn Met Glu Ser Val Pro Leu His Leu
	165                      170                      175
	Ser Leu Thr Glu Thr Gln Ser Gln Gly Leu Cys Leu Arg Arg His Pro
	180                      185                      190
60	



550

Lys Lys Lys Lys  
195

5

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

15 Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg Lys  
1 5 10 15

Arg Leu Leu Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu  
20 25 30

20 Ala Xaa Xaa Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp  
35 40 45

Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr  
50 55 60

25 Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val  
65 70 75 80

Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val  
85 90 95

30 Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys  
100 105 110

35 Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp  
115 120 125

Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln  
130 135 140

40 Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala  
145 150 155 160

Ala Arg Xaa His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg  
165 170 175

45 Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser Met  
180 185 190

50 Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln Asn  
195 200 205

Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu Ala  
210 215 220

55 Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly Pro  
225 230 235 240

Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa  
245 250

60

## (2) INFORMATION FOR SEQ ID NO: 326:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val  
 1 5 10 15

15

Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Pro Ala  
 20 25 30

20

Val Ile Lys Asn Asn Ser His Tyr Gln Thr Ser Lys Ala Leu Glu Leu  
 35 40 45

Glu Lys Thr Thr Glu Asn Lys Glu Ser Asn Pro Phe Ile Leu Gln Val  
 50 55 60

25

Asn Lys Leu Xaa  
 65

## (2) INFORMATION FOR SEQ ID NO: 327:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Gly Glu Gly Lys Asn Gly Phe Gly Gly Phe Val His Thr Ala Asp  
 1 5 10 15

40

Ala Cys Trp Glu Gly Val His Ser Glu Pro Val Cys Arg Thr Val His  
 20 25 30

Thr Val His Thr Cys His His Gln Ala Phe Leu Val Leu Ile Gly Trp  
 35 40 45

45

Ser Lys Ser Gly Lys Glu Arg Lys Glu Ala Phe Leu Thr Ala Ile Ile  
 50 55 60

50

Leu Asn Ser Arg Ser Ile His Ile Ser Cys Ser Trp Pro Pro Ser Pro  
 65 70 75 80

Val Pro Gln Xaa

55

## (2) INFORMATION FOR SEQ ID NO: 328:

60

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

5 Met Leu Leu Ile Asn Leu Leu Trp Leu Val Thr Met Ile Lys Ser Val  
     1                    5                    10                    15  
 Ile Asn Asn Asn Ile Ile Leu Phe Leu Lys Lys Lys Ser Leu Phe Phe  
                     20                    25                    30  
 10 Ile Asp Ser Val  
             35

15

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 63 amino acids  
 20 (B) TYPE: amino acid  
     (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

25 Met Thr Phe Pro Phe Glu Lys Lys Ile Val Ala Phe Ser Ala Phe Tyr  
     1                    5                    10                    15  
 Leu Ile Pro Gly Glu Ser Arg Leu Ala Pro Thr Phe Asn Pro Ser Ala  
                     20                    25                    30  
 30 Asp Met Thr Val Ile Leu Arg Gly Arg Ala Gln His Lys Thr Ala Met  
             35                    40                    45  
 Leu Glu Ser Tyr Asn Trp Lys Val Ser Cys Gln Leu Arg Glu Xaa  
     50                    55                    60

35

(2) INFORMATION FOR SEQ ID NO: 330:

40 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 35 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear  
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met His Ser Lys Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile  
     1                    5                    10                    15  
 50 Leu Ile Leu Pro Val Cys Ala His Leu His Glu Glu Leu Asn Cys Cys  
                     20                    25                    30  
 Phe His Arg  
             35

55

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:  
 60 (A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

5 Met Gly Ala Leu Val Leu Leu Leu Cys Leu Leu Val Gly Val Gln Gln  
 1 5 10 15

Ser Gly Ser Val Trp Asp Ser  
 20

10

(2) INFORMATION FOR SEQ ID NO: 332:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

20

Met Gln Ser Ala Glu Ile Leu Ser Trp Thr Asp Val Leu His Asp Phe  
 1 5 10 15

25 Leu Phe Ser Leu Phe Leu Trp Pro Ala Phe Glu Asp Arg Ala Leu Leu  
 20 25 30

Ile Phe Thr Leu Asn Gln Ile Val  
 35 40

30

(2) INFORMATION FOR SEQ ID NO: 333:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

40 Met Gln Ser Leu Val Gln Trp Gly Leu Asp Ser Tyr Asp Tyr Leu Gln  
 1 5 10 15

Asn Ala Pro Pro Gly Phe Phe Pro Arg Leu Gly Val Ile Gly Phe Ala  
 20 25 30

45

Gly Leu Ile Gly Leu Leu Leu Ala Arg Gly Ser Lys Ile Lys Lys Leu  
 35 40 45

50 Val Tyr Pro Pro Gly Phe Met Gly Leu Ala Ala Ser Leu Tyr Tyr Pro  
 50 55 60

Gln Gln Ala Ile Val Phe Ala Gln Val Ser Gly Glu Arg Leu Tyr Asp  
 65 70 75 80

55 Trp Gly Leu Arg Gly Tyr Ile Val Ile Glu Asp Leu Trp Lys Glu Asn  
 85 90 95

Phe Gln Lys Pro Gly Asn Val Lys Asn Ser Pro Gly Thr Lys Xaa  
 100 105 110

60

## (2) INFORMATION FOR SEQ ID NO: 334:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Ala Pro Ser Leu Leu Leu Ala Pro Leu Cys Ser Leu Glu Ala  
 1 5 10 15

15

Val Leu Ser Ser Pro Leu Glu Lys Gln Cys Gln Leu Pro Gly Ile Phe  
 20 25 30

Cys Gln Leu Gln Leu Pro Cys Pro Leu Leu Leu Ser Ala Gln Leu Leu  
 35 40 45

20

Lys Gly Ile Val Xaa Pro Arg Cys Pro Ala Ser Leu Pro Gln Pro Pro  
 50 55 60

25

His Pro Ala Pro Ser Trp His Leu Pro Leu His Cys Thr Glu Arg Xaa  
 65 70 75 80

Pro His His Leu Pro Leu Gln Gly Gly Ser Ser Asn Met Glu Glu Xaa  
 85 90 95

30

Asn Tyr Arg Gly Tyr Xaa Asp Ala Gln Leu  
 100 105

35

## (2) INFORMATION FOR SEQ ID NO: 335:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Thr Thr Cys Leu Phe Gly Leu Leu Ser Cys Glu Met Ser Ala Gln  
 1 5 10 15

45

Val Ser Gln Lys Ser Cys Val Tyr Asp Glu Ser Glu Cys Phe Ser Ser  
 20 25 30

Val Gly Gln Leu Leu Ala Leu Leu Ile Leu Val Tyr Val Leu Pro Ser  
 35 40 45

50

Ile Xaa  
 50

55

## (2) INFORMATION FOR SEQ ID NO: 336:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

5 Met Leu Trp Lys Cys Ser Gln Asn Ile Ala Arg Cys Leu Leu Leu  
 1 5 10 15

Leu Ala Leu Val Glu Ile Lys Leu Glu Asp Leu Gln Ser Gln Leu His  
 20 25 30

10 Pro Thr Trp Lys Ser Ile Pro Gly Pro Ser Pro Arg Asn Gln His Arg  
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 337:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

25

Met Leu Ile Pro Leu Gln Cys Leu Phe Ser Ser Asp Arg Met Leu Thr  
 1 5 10 15

30

Phe Leu Thr Pro Trp Gln Lys Gly Glu Lys Cys Val Leu Gly Trp Val  
 20 25 30

Thr Lys Phe Leu Ser Glu Ile Ser Xaa  
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 338:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

45

Met Thr Phe Ser Ser Leu Lys Leu Phe Val Leu Thr Cys Ile Ile Lys  
 1 5 10 15

50

Gly Leu Glu Arg Phe Ile Ile Leu Arg Glu Val Cys Asn Gln Glu Ile  
 20 25 30

Gln Arg Ser Leu Ser Ser Asn Leu Val His Val Leu Leu Gln Pro Ala  
 35 40 45

55

Thr Phe Lys Asp Val Leu Val Thr Glu Ile Ile Cys Leu Cys Met Cys  
 50 55 60

Leu Tyr Ser Ile Lys Tyr Met Pro Pro Gln Lys Lys  
 65 70 75

60

## (2) INFORMATION FOR SEQ ID NO: 339:

## 5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

10 Lys Val Tyr Ile Phe Leu Ile Phe Met Val Leu Ile Leu Pro Ser Leu  
1 5 10 15  
Gly Leu Thr Arg Tyr Met Pro Pro Xaa Ser Xaa Leu Asn Ser Glu  
20 25 30  
15

## (2) INFORMATION FOR SEQ ID NO: 340:

## 20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

25 Met Ala Lys Ile Ser Pro Phe Glu Val Val Lys Arg Thr Ser Val Pro  
1 5 10 15  
30 Val Leu Val Gly Leu Val Ile Val Ile Val Ala Thr Glu Leu Met Val  
20 25 30  
Pro Gly Thr Ala Ala Ala Val Thr Gly Lys  
35 40  
35

## (2) INFORMATION FOR SEQ ID NO: 341:

## 40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

45 Met Arg Leu Phe Phe Ile Gly Phe Leu Leu Leu Phe Ser Phe Gly Leu  
1 5 10 15  
Leu Arg Gln Pro Ser Leu Ser Ala Glu His  
20 25  
50

## (2) INFORMATION FOR SEQ ID NO: 342:

## 55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

60

Met Val Phe Ser Val Ser Ser Ala Leu Ala Leu Leu Met Leu Leu  
 1 5 10 15  
 5 Arg Ser Ser Asp Leu Ala Lys Lys Thr Glu  
 20 25

10 (2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 157 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Ser Leu Glu Phe Tyr Gln Lys Lys Lys Ser Arg Trp Pro Phe Ser  
 1 5 10 15  
 20 Asp Glu Cys Ile Pro Trp Glu Val Trp Thr Val Lys Val His Val Val  
 20 25 30  
 Ala Leu Ala Thr Glu Gln Glu Arg Gln Ile Cys Arg Glu Lys Val Gly  
 35 40 45  
 25 Glu Lys Leu Cys Glu Lys Ile Ile Asn Ile Val Glu Val Met Asn Arg  
 50 55 60  
 His Glu Tyr Leu Pro Lys Met Pro Thr Gln Ser Glu Val Asp Asn Val  
 30 65 70 75 80  
 Phe Asp Thr Gly Leu Arg Asp Val Gln Pro Tyr Leu Tyr Lys Ile Ser  
 85 90 95  
 35 Phe Gln Ile Thr Asp Ala Leu Gly Thr Ser Val Thr Thr Thr Met Arg  
 100 105 110  
 Arg Leu Ile Lys Asp Thr Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly  
 115 120 125  
 40 Ser Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu  
 130 135 140  
 Gly Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp Xaa  
 45 145 150 155

50 (2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 520 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Phe Leu Leu Pro Leu Pro Ala Ala Gly Arg Val Val Val Arg Arg  
 1 5 10 15  
 60 Leu Ala Val Arg Arg Phe Gly Ser Arg Ser Leu Ser Thr Ala Asp Met



	20	25	30
	Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp Asp		
	35	40	45
5	Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu Ala		
	50	55	60
10	Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys Ala		
	65	70	75
	Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser Val		
	85	90	95
15	Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln Glu		
	100	105	110
	Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala Gly		
	115	120	125
20	Cys Arg Gln Ile Gln Asp Leu Glu Leu Ser Ser Val Glu Val Asp Pro		
	130	135	140
25	Cys Gly Asp Ala Gln Ala Ala Ala Glu Gly Ala Val Leu Gly Leu Tyr		
	145	150	155
	Glu Tyr Asp Asp Leu Lys Gln Lys Lys Lys Met Ala Val Ser Ala Lys		
	165	170	175
30	Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu Phe		
	180	185	190
	Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala Asn		
	195	200	205
35	Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu Lys		
	210	215	220
40	Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp Ile		
	225	230	235
	Glu Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser Asp		
	245	250	255
45	Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn Ala		
	260	265	270
	Asn Glu Pro Pro Leu Val Phe Val Gly Lys Gly Ile Thr Phe Asp Ser		
	275	280	285
50	Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg Ala		
	290	295	300
55	Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala Ala		
	305	310	315
	Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys Glu		
	325	330	335
60	Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg Ala		

559

340                      345                      350  
 Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly Arg  
                     355                      360                      365  
 5    Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro Lys  
                     370                      375                      380  
 10    Xaa Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala Leu  
                     385                      390                      395                      400  
 Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp Asn  
                     405                      410                      415  
 15    Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg Met  
                     420                      425                      430  
 Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu Ala  
                     435                      440                      445  
 20    Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr Ala  
                     450                      455                      460  
 Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His Leu  
 25    465                      470                      475                      480  
 Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu Arg  
                     485                      490                      495  
 30    Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu Leu  
                     500                      505                      510  
 Arg Phe Ser Gln Asp Asn Ala Xaa  
                     515                      520

35

(2) INFORMATION FOR SEQ ID NO: 345:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

45

Thr Ile Leu Phe Leu Phe Leu Gln Leu Ser Ala Leu Arg Leu Ile Val  
                     1                      5                      10                      15

50

Gly Lys Asp Ser Ile Asp Ile Asp Ile Ser Ser Arg Arg Arg Glu Asp  
                     20                      25                      30

Gln Ser Leu Arg Leu Asn Ala  
                     35

55

(2) INFORMATION FOR SEQ ID NO: 346:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

560

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

5 Met Thr Ser Glu Leu Asp Ile Phe Val Gly Asn Thr Thr Leu Ile Asp  
     1                    5                    10                    15  
 Glu Asp Val Tyr Arg Leu Trp Leu Asp Gly Tyr Ser Val Thr Asp Ala  
                     20                    25                    30  
 10 Val Ala Leu Arg Val Arg Ser Gly Ile Leu Glu Gln Thr Gly Ala Thr  
             35                    40                    45  
 Ala Ala Val Leu Gln Ser Asp Thr Met Asp His Tyr Arg Thr Phe His  
 15            50                    55                    60  
 Met Leu Glu Arg Leu Leu His Ala Pro Pro Lys Leu Leu His Gln Leu  
     65                    70                    75                    80  
 20 Ile Phe Gln Ile Pro Pro Ser Arg Gln Ala Leu Leu Ile Glu Arg Tyr  
                     85                    90                    95  
 Tyr Ala Phe Asp Glu Ala Phe Val Arg Glu Val Leu Gly Lys Lys Leu  
             100                    105                    110  
 25 Ser Lys Gly Thr Lys Lys Asp Leu Asp Asp Ile Ser Thr Lys Thr Gly  
             115                    120                    125  
 Ile Thr Leu Lys Ser Cys Arg Arg Gln Phe Asp Asn Phe Lys Arg Val  
 30            130                    135                    140  
 Phe Lys Val Val Glu Glu Met Arg Gly Ser Leu Val Asp Asn Ile Gln  
     145                    150                    155                    160  
 35 Gln His Phe Leu Leu Ser Asp Arg Leu Ala Arg Asp Tyr Ala Ala Ile  
             165                    170                    175  
 Val Phe Phe Ala Asn Asn Arg Phe Glu Thr Gly Lys Lys Lys Leu Gln  
             180                    185                    190  
 40 Tyr Leu Ser Phe Gly Asp Phe Ala Phe Cys Ala Glu Leu Met Ile Gln  
             195                    200                    205  
 Asn Trp Thr Leu Gly Pro Val Asp Ser Gln Met Asp Asp Met Asp Met  
 45            210                    215                    220  
 Asp Leu Asp Arg Asn Phe Ser Arg Thr Xaa  
     225                    230

50

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

60 Met Ala Ala Ala Val Ala Gly Met Leu Arg Gly Gly Leu Leu Pro Gln

1                      5                      10                      15

Ala Gly Arg Leu Pro Thr Leu Gln Thr Val Arg Tyr Gly Ser Lys Ala  
20                      25                      30

5 Val Thr Arg His Arg Arg Val Met His Phe Gln Arg Gln Lys Leu Met  
35                      40                      45

Ala Val Thr Glu Tyr Ile Pro Pro Lys Pro Ala Ile His Pro Ser Cys  
10 50                      55                      60

Leu Pro Ser Pro Pro Ser Pro Pro Gln Glu Glu Ile Gly Leu Ile Arg  
65                      70                      75                      80

15 Leu Leu Arg Arg Glu Ile Ala Ala Val Phe Gln Asp Asn Arg Met Ile  
85                      90                      95

Ala Val Cys Gln Asn Val Ala Leu Ser Ala Glu Asp Lys Leu Leu Ile  
100                      105                      110

20 Ala Thr Pro Ala Ala Glu Thr Gln Asp Pro Asp Glu Gly Leu Pro Gln  
115                      120                      125

Pro Gly Pro Glu Ser Pro Ser Trp Arg Ile Pro Ser Thr Lys Ile Cys  
25 130                      135                      140

Cys Pro Phe Leu Trp Gly Thr Thr Cys Cys Trp Ser Val Lys Ser Pro  
145                      150                      155                      160

30 Arg Ser Arg Arg Trp Tyr Gly Ser Xaa  
165

35 (2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Lys Arg Ser Phe Leu Leu Pro Leu Leu Leu Val Gly Phe Leu Asp  
1                      5                      10                      15

45 Thr Ala His Leu Ile Leu Leu Glu Thr Leu Ser Val Cys Leu Trp Leu  
20                      25                      30

Pro Ser Leu Ile Asp Ser Arg Cys Val Met Ser  
50 35                      40

55 (2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Lys Glu Gly Pro Pro Cys Lys Arg His His Tyr Tyr Gln Asn Cys  
 1 5 10 15  
 5 Gly Ala Lys Leu Leu Val Ser Leu Phe Gly Glu Thr Asn Gln Ile His  
 20 25 30  
 Leu Leu Glu Thr Gln Val Gly Thr Glu Lys Gly Gly Glu Arg Ile Trp  
 35 40 45  
 10 Glu Glu Lys Trp Arg Ile Ser Ser Thr Val Leu Phe Ile Ser Val Asn  
 50 55 60  
 Ser Tyr Val Glu Gly Ser Val Leu Glu Ile Lys Leu Phe Tyr  
 15 65 70 75

20 (2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Ser Glu Ile Leu Ser Leu Leu Phe Cys Leu Leu Gly Pro Ala Leu  
 1 5 10 15  
 30 Asp Glu Arg Arg Glu Glu Lys Asp  
 20

35 (2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu  
 1 5 10 15  
 45 Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser  
 20 25 30  
 Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu  
 50 35 40 45  
 Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val  
 50 55 60  
 55 Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu  
 65 70 75 80  
 Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly  
 85 90 95  
 60

563

Arg Pro Ala Gly Gly Ala His Leu Cys Ala Met Xaa Val Ile Glu Gly  
 100 105 110  
 5 Leu Val Val Asp Val Gly Glu Arg Ile Leu His Gly Gln Arg Glu Val  
 115 120 125  
 Gly Gln Val Ser Gln Val Leu Pro Ala Leu Ser Leu Gly Leu Val Phe  
 130 135 140  
 10 Leu Cys Gln Gly Thr Val Glu Lys Val Ser Gly Ala Ala His Cys Ser  
 145 150 155 160  
 Ser Leu Leu Cys Cys Leu Pro Trp Gln Cys Ser Gly Gly Gly Phe Pro  
 165 170 175  
 15 Thr Xaa Arg Cys Ser Arg Pro Tyr Phe Ser Ser His Lys Gly Val Ala  
 180 185 190  
 Ala Thr Leu Ala Leu Thr Cys His Cys Asp Lys Val His Val Ala Gly  
 195 200 205  
 20 Leu Gly Lys Asp Trp Ala Ile Glu Gln Arg Arg Arg Thr Cys Glu Ser  
 210 215 220  
 25 Asp Xaa Glu Xaa Xaa Pro Phe Thr Leu Ala Gly Leu Val Leu Val Leu  
 225 230 235 240  
 Arg Phe Cys Gln Val Val Leu Val Trp Ile Pro Gln Leu Gly Asp Lys  
 245 250 255  
 30 His Trp Arg Gly Met Thr Arg Leu Gly Arg Val Ser Leu Thr Ser Ser  
 260 265 270  
 35 Ile Xaa

40 (2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Ile Phe Thr Ser Val Thr Lys Gly Ile Leu Leu Ile Ala Leu Trp  
 1 5 10 15  
 50 Val Pro Leu Phe His Phe Met Leu Ile Asp Ser Ile Leu Gly Pro Ser  
 20 25 30  
 Arg Leu Leu Thr Asp Gly Val Pro Phe Asn Pro Trp His Val Xaa  
 35 40 45  
 55

(2) INFORMATION FOR SEQ ID NO: 353:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

5

Met Lys Thr

1

10

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

20

Met Ser Ile Ser Gly Thr Asp Gly Leu Ile Leu Leu Val Gly Leu  
1 5 10 15Glu Ala Xaa Val Arg Ser Ser Lys Lys Trp Ile Pro Lys Ala Leu Xaa  
20 25 30

25

Val Thr Gln Ala Lys Trp Asn Ser Trp Pro Ser Arg Arg Asn Ala Gly  
35 40 45Phe Ala Leu His  
50

30

(2) INFORMATION FOR SEQ ID NO: 355:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

40

Met Glu His Cys Leu Tyr His Ser Val His Gly Ile Asn Pro Tyr Ile  
1 5 10 15

45

His Lys Asn Thr His Pro Ser Ile Asn Ile Tyr Met Val Trp Asp Glu  
20 25 30Gln Val Asn Ser Phe Glu Arg Glu Phe Val Pro Phe Phe Phe Leu Ile  
35 40 45

50

Ile Leu Leu Asn Cys Cys Gln Leu Ser Asn Lys Gln Thr Glu Lys Leu  
50 55 60Phe Gly Lys Thr Leu His Thr Pro Phe Leu Ser Ser Ala Leu Lys Tyr  
65 70 75 80

55

Arg Leu Asn Thr His Ile Leu Pro Val Phe Ser Tyr Ser Asp Ser Ile  
85 90 95

60

Leu Thr Cys His Leu Ile Leu Ala Ser Tyr Phe Ser His Val Tyr Leu  
100 105 110

Pro Val Thr Cys Ile Cys Tyr Leu Asn Arg Lys Lys Asn Ile Gln Lys  
115 120 125

5 Lys Lys Asn Xaa  
130

10 (2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly Ser Arg Asp His Leu Phe Lys Val Leu Val Val Gly Asp Ala  
1 5 10 15

20 Ala Val Gly Lys Thr Ser Leu Val Gln Asp Tyr Ser Gln Asp Ser Phe  
20 25 30

25 Ser Lys His Tyr Lys Ser Thr Val Gly Val Asp Phe Ala Leu Lys Val  
35 40 45

Leu Gln Trp Ser Asp Tyr Glu Ile Val Arg Leu Gln Leu Trp Asp Ile  
50 55 60

30 Ala Gly Gln Glu Arg Phe Thr Ser Met Thr Arg Leu Tyr Tyr Arg Asp  
65 70 75 80

Ala Ser Ala Cys Val Ile Met Phe Asp Val Thr Asn Ala Thr Thr Phe  
85 90 95

35 Ser Asn Ser Gln Arg Trp Lys Gln Asp Leu Asp Ser Lys Leu Thr Leu  
100 105 110

40 Pro Asn Gly Glu Pro Val Pro Cys Leu Leu Leu Ala Asn Lys Cys Asp  
115 120 125

Leu Ser Pro Trp Ala Val Ser Arg Asp Gln Ile Asp Arg Phe Ser Lys  
130 135 140

45 Glu Asn Gly Phe Thr Gly Trp Thr Glu Thr Ser Val Lys Glu Asn Lys  
145 150 155 160

Asn Ile Asn Glu Ala Met Arg Val Leu Ile Glu Lys Met Met Arg Asn  
165 170 175

50 Ser Thr Glu Asp Ile Met Ser Leu Ser Thr Gln Gly Asp Tyr Ile Asn  
180 185 190

55 Leu Gln Thr Lys Ser Ser Ser Trp Ser Cys Cys Xaa  
195 200

60 (2) INFORMATION FOR SEQ ID NO: 357:



## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ile Ser Leu Ile Phe Gln Leu Glu Glu Glu Lys Leu Val Glu Lys  
 1 5 10 15

10 Phe Phe Phe Phe Leu Phe Phe Phe Leu Lys Lys Gly Ser Gln Gly Ser  
 20 25 30

Asn Leu Lys Ile Val Pro Arg His Met Arg Val Val Leu Arg Gly  
 35 40 45

15

## (2) INFORMATION FOR SEQ ID NO: 358:

## 20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Thr Tyr Val Thr Cys Leu His Val Cys Leu Leu Val Glu Phe Leu  
 1 5 10 15

30 Asn Ser Gln Leu Thr Asn His Arg Lys Tyr Tyr Phe Leu Ser Tyr Gly  
 20 25 30

Phe Trp Phe Thr Gly Leu Arg Gly Phe Ser Glu Tyr Leu Trp Pro Gln  
 35 40 45

35 Gln His Thr Ser Phe His Pro Asn Arg Asn Glu Ile Asn Phe Val Ser  
 50 55 60

Thr Asp Asn Arg Ile Trp Val Thr Xaa  
 65 70

40

## (2) INFORMATION FOR SEQ ID NO: 359:

## 45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Ser Asp Gln Glu Ala Lys Pro Ser Thr Glu Asp Leu Gly Asp Lys  
 1 5 10 15

55 Lys Glu Gly Glu Tyr Ile Lys Leu Lys Val Ile Gly Gln Asp Ser Ser  
 20 25 30

Glu Ile His Phe Lys Val Lys Met Thr Thr His Leu Lys Lys Leu Lys  
 35 40 45

60 Glu Ser Tyr Cys Gln Arg Gln Gly Val Pro Met Asn Ser Leu Arg Phe

	50		55		60	
	Leu Phe Glu Gly Gln Arg Ile Ala Asp Asn His Thr Pro Lys Glu Leu					
5	65		70		75	80
	Gly Met Glu Glu Glu Asp Val Ile Glu Val Tyr Gln Glu Gln Thr Gly					
		85		90		95
10	Gly His Ser Thr Val Xaa					
		100				

(2) INFORMATION FOR SEQ ID NO: 360:

## 15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Gly Phe Pro Gln Trp His Leu Gly Asn His Ala Val Glu Pro Val  
1 5 10 15

25

Thr Ser Ile Leu Leu Leu Phe Leu Leu Met Met Leu Gly Val Arg Gly  
20 25 30

Leu Leu Leu Val Gly Leu Val Tyr Leu Val Ser His Leu Ser Gln Arg  
35 40 45

30

## 35

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu  
1 5 10 15

Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His  
20 25 30

50

Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu Asp  
35 40 45

Met Pro Asn Val Arg Glu Leu Ala Glu Ser Asp Phe Ala Ser Thr Phe  
50 55 60

55

Arg Leu Leu Thr Val Phe Ala Tyr Gly Thr Tyr Ala Asp Tyr Leu Ala  
65 70 75 80

Glu Ala Arg Asn Leu Pro Pro Leu Thr Glu Ala Gln Lys Asn Lys Leu  
85 90 95

60

Arg His Leu Ser Val Val Thr Leu Ala Ala Lys Val Lys Cys Ile Pro  
 100 105 110

5 Tyr Ala Val Leu Leu Glu Ala Leu Ala Leu Arg Asn Val Arg Gln Leu  
 115 120 125

Glu Asp Leu Val Ile Glu Ala Val Tyr Ala Asp Val Leu Arg Gly Ser  
 130 135 140

10 Leu Asp Gln Arg Asn Gln Arg Leu Glu Val Asp Tyr Ser Ile Gly Arg  
 145 150 155 160

15 Asp Ile Gln Arg Gln Asp Leu Ser Ala Ile Ala Arg Thr Leu Xaa Lys  
 165 170 175

Asn His Xaa

20

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

30 Met Lys Ser Ser Ser Leu Phe Phe Phe Phe Leu Ala His Phe Ile His  
 1 5 10 15

Ser His Asp Leu Pro Gly Leu Cys Arg  
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 363:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 224 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

45

Met Lys Phe Ala Ala Ser Gly Xaa Phe Leu His His Met Ala Gly Leu  
 1 5 10 15

50

Ser Ser Ser Lys Leu Ser Met Ser Lys Ala Leu Pro Leu Thr Lys Val  
 20 25 30

Val Gln Asn Asp Ala Tyr Thr Ala Pro Ala Leu Pro Ser Ile Arg  
 35 40 45

55

Thr Lys Ala Leu Thr Asn Met Ser Arg Thr Leu Val Asn Lys Glu Glu  
 50 55 60

Pro Pro Lys Glu Leu Pro Ala Ala Glu Pro Val Leu Ser Pro Leu Glu  
 65 70 75 80

60

Gly Thr Lys Met Thr Val Asn Asn Leu His Pro Arg Val Thr Glu Glu  
                                     85                                    90                                    95  
 5 Asp Ile Val Glu Leu Phe Cys Val Cys Gly Ala Leu Lys Arg Ala Arg  
                                     100                                    105                                    110  
 Leu Val His Pro Gly Val Ala Glu Val Val Phe Val Lys Lys Asp Asp  
                                     115                                    120                                    125  
 10 Ala Ile Thr Ala Tyr Lys Lys Tyr Asn Asn Arg Cys Leu Asp Gly Gln  
                                     130                                    135                                    140  
 Pro Met Lys Cys Asn Leu His Met Asn Gly Asn Val Ile Thr Ser Asp  
 15 145                                    150                                    155                                    160  
 Gln Pro Ile Leu Leu Arg Leu Ser Asp Ser Pro Ser Met Lys Lys Glu  
                                     165                                    170                                    175  
 Ser Glu Leu Pro Arg Arg Val Asn Ser Ala Ser Ser Ser Asn Pro Pro  
 20 180                                    185                                    190  
 Ala Glu Val Asp Pro Asp Thr Ile Leu Lys Ala Leu Phe Lys Ser Ser  
                                     195                                    200                                    205  
 25 Gly Ala Ser Xaa Thr Thr Gln Pro Thr Glu Phe Lys Ile Lys Leu Xaa  
                                     210                                    215                                    220

30

(2) INFORMATION FOR SEQ ID NO: 364:

- 35 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 349 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

40 Met Ser Lys Asn Cys Ile Lys Leu Leu Cys Glu Asp Pro Val Phe Ala  
     1                                    5                                    10                                    15  
 45 Glu Tyr Ile Lys Cys Ile Leu Met Asp Glu Arg Thr Phe Leu Asn Asn  
                                     20                                    25                                    30  
 Asn Ile Val Tyr Thr Phe Met Thr His Phe Leu Leu Lys Val Gln Ser  
                                     35                                    40                                    45  
 50 Gln Val Phe Ser Glu Ala Asn Cys Ala Asn Leu Ile Ser Thr Leu Ile  
                                     50                                    55                                    60  
 Thr Asn Leu Ile Ser Gln Tyr Gln Asn Leu Gln Ser Asp Phe Ser Asn  
 55 65                                    70                                    75                                    80  
 Arg Val Glu Ile Ser Lys Ala Ser Ala Ser Leu Asn Gly Asp Leu Arg  
                                     85                                    90                                    95  
 60 Ala Leu Ala Leu Leu Leu Ser Val His Thr Pro Lys Gln Leu Asn Pro  
                                     100                                    105                                    110

Ala Leu Ile Pro Thr Leu Gln Glu Leu Leu Ser Lys Cys Arg Thr Cys  
 115 120 125

5 Leu Gln Gln Arg Asn Ser Leu Gln Glu Gln Glu Ala Lys Glu Arg Lys  
 130 135 140

Thr Lys Asp Asp Glu Gly Ala Thr Pro Ile Lys Arg Arg Arg Val Ser  
 145 150 155 160

10 Ser Asp Glu Glu His Thr Val Asp Ser Cys Ile Ser Asp Met Lys Thr  
 165 170 175

Glu Thr Arg Glu Val Leu Thr Pro Thr Ser Thr Ser Asp Asn Glu Thr  
 15 180 185 190

Arg Asp Ser Ser Ile Ile Asp Pro Gly Thr Glu Gln Asp Leu Pro Ser  
 195 200 205

20 Pro Glu Asn Ser Ser Val Lys Glu Tyr Arg Met Glu Val Pro Ser Ser  
 210 215 220

Phe Ser Glu Asp Met Ser Asn Ile Arg Ser Gln His Ala Glu Glu Gln  
 225 230 235 240

25 Ser Asn Asn Gly Arg Tyr Asp Asp Cys Lys Glu Phe Lys Asp Leu His  
 245 250 255

Cys Ser Lys Asp Ser Thr Leu Ala Glu Glu Glu Ser Glu Phe Pro Ser  
 30 260 265 270

Thr Ser Ile Ser Ala Val Leu Ser Asp Leu Ala Asp Leu Arg Ser Cys  
 275 280 285

35 Asp Gly Gln Ala Leu Pro Ser Gln Asp Pro Glu Val Ala Leu Ser Leu  
 290 295 300

Ser Cys Gly His Ser Arg Gly Leu Phe Ser His Met Gln Gln His Asp  
 305 310 315 320

40 Ile Leu Asp Thr Leu Cys Arg Thr Ile Glu Ser Thr Ile His Val Val  
 325 330 335

Thr Arg Ile Ser Gly Lys Gly Asn Gln Ala Ala Ser Xaa  
 45 340 345

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Leu His Gln Asp His Ile Thr Phe Ala Met Leu Leu Ala Arg Ile  
 1 5 10 15

60 Lys Leu Lys Gly Thr Val Gly Glu Pro Thr Tyr Asp Ala Glu Phe Gln

	20	25	30
	His Phe Leu Arg Gly Asn Glu Ile Val Leu Ser Ala Gly Ser Thr Pro		
5	35	40	45
	Arg Ile Gln Gly Leu Thr Val Glu Gln Ala Glu Ala Val Val Arg Leu		
	50	55	60
10	Ser Cys Leu Pro Ala Phe Lys Asp Leu Ile Ala Lys Val Gln Ala Asp		
	65	70	75 80
	Glu Gln Phe Gly Ile Trp Leu Asp Ser Ser Ser Pro Glu Gln Thr Val		
	85	90	95
15	Pro Tyr Leu Trp Ser Glu Glu Thr Pro Ala Thr Pro Ile Gly Gln Ala		
	100	105	110
	Ile His Arg Leu Leu Leu Ile Gln Ala Phe Arg Pro Asp Arg Leu Leu		
20	115	120	125
	Ala Met Ala His Met Phe Val Ser Thr Asn Leu Gly Glu Ser Phe Met		
	130	135	140
25	Ser Ile Met Glu Gln Pro Leu Asp Leu Thr His Ile Val Xaa Thr Glu		
	145	150	155 160
	Val Lys Pro Asn Thr Pro Val Leu Met Cys Ser Val Pro Gly Tyr Asp		
	165	170	175
30	Ala Ser Gly His Val Glu Asp Leu Ala Ala Glu Gln Asn Thr Gln Ile		
	180	185	190
	Thr Ser Ile Ala Ile Gly Ser Ala Glu Gly Phe Asn Gln Ala Asp Lys		
35	195	200	205
	Ala Ile Asn Thr Ala Val Lys Ser Gly Arg Trp Val Met Leu Lys Asn		
	210	215	220
40	Val His Leu Ala Pro Gly Trp Leu Met Gln Leu Glu Lys Lys Leu His		
	225	230	235 240
	Ser Leu Gln Pro His Ala Cys Phe Arg Leu Phe Leu Thr Met Glu Ile		
	245	250	255
45	Asn Pro Lys Val Pro Val Asn Leu Leu Arg Ala Gly Arg Ile Phe Val		
	260	265	270
	Phe Glu Pro Pro Pro Gly Xaa Lys Ala Asn Met Leu Arg Thr Phe Ser		
50	275	280	285
	Ser Ile Pro Val Ser Arg Ile Cys Lys Ser Pro Asn Glu Arg Ala Arg		
	290	295	300
55	Leu Tyr Phe Leu Leu Ala Trp Phe His Ala Ile Ile Gln Glu Arg Leu		
	305	310	315 320
	Arg Tyr Ala Pro Leu Gly Trp Ser Lys Lys Tyr Glu Phe Gly Glu Ser		
	325	330	335
60	Asp Leu Arg Ser Xaa Cys Asp Thr Val Asp Thr Trp Leu Asp Asp Thr		

340 345 350

Ala Lys Gly Arg Gln Asn Ile Ser Pro Asp Lys Ile Pro Trp Ser Ala  
355 360 365

5 Leu Lys Thr Leu Met Ala Gln Ser Ile Tyr Gly Gly Arg Val Asp Asn  
370 375 380

10 Glu Phe Asp Gln Arg Leu Leu Asn Thr Phe Leu Glu Arg Leu Phe Thr  
385 390 395 400

Thr Arg Ser Phe Asp Ser Glu Phe Lys Leu Ala Cys Lys Val Asp Gly  
405 410 415

15 His Lys Asp Ile Gln Met Pro Asp Gly Met Gln Ala Arg Gly Val Cys  
420 425 430

Ala Val Gly Gly Val Ala Pro Arg His Pro Asp Ala Leu Leu Ala Gly  
435 440 445

20 Pro Ala Gln Gln Arg Arg Glu Ser Pro Pro Tyr His Thr Gly Cys Gly  
450 455 460

25 His Asp Gln  
465

30 (2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Ala Asp Glu Ala Thr Arg Arg Val Val Ser Glu Ile Pro Val Leu  
1 5 10 15

40 Lys Thr Asn Ala Gly Pro Arg Asp Arg Glu Leu Trp Val Gln Arg Leu  
20 25 30

Lys Glu Glu Tyr Gln Ser Leu Ile Arg Tyr Val Glu Asn Asn Lys Asn  
35 40 45

45 Ala Asp Asn Asp Trp Phe Arg Leu Glu Ser Asn Lys Glu Gly Thr Arg  
50 55 60

50 Trp Phe Gly Lys Cys Trp Tyr Ile His Asp Leu Leu Lys Tyr Glu Phe  
65 70 75 80

Asp Ile Glu Phe Asp Ile Pro Ile Thr Tyr Pro Thr Thr Ala Pro Glu  
85 90 95

55 Ile Ala Val Pro Glu Leu Asp Gly Lys Thr Ala Lys Met Tyr Arg Gly  
100 105 110

Gly Lys Ile Cys Leu Thr Asp His Phe Lys Pro Leu Trp Gly Gln Glu  
115 120 125

60

Cys Ala Gln Ile Trp Thr Ser Ser Ser His Gly Ser Gly Ala Gly Ser  
130 135 140

5 Met Xaa Gly Ser Gly Asn Pro Xaa  
145 150

(2) INFORMATION FOR SEQ ID NO: 367:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Tyr Asp Gly Thr Lys Glu Val Pro Met Asn Pro Val Lys Ile Tyr  
1 5 10 15

20 Gln Val Cys Asp Ile Pro Gln Pro Gln Gly Ser Ile Ile Asn Pro Gly  
20 25 30

Ser Thr Gly Ser Ala Pro Trp Asp Glu Lys Asp Asn Asp Val Asp Glu  
35 40 45

25

Glu Asp Glu Glu Asp Glu Leu Asp Gln Ser Gln His His Val Pro Ile  
50 55 60

30 Gln Asp Thr Phe Pro Phe Leu Asn Ile Asn Gly Ser Pro Met Ala Pro  
65 70 75 80

Ala Ser Val Gly Asn Cys Ser Val Gly Asn Cys Ser Pro Glu Ala Val  
85 90 95

35 Trp Pro Lys Thr Glu Pro Leu Glu Met Glu Val Pro Gln Ala Pro Ile  
100 105 110

Gln Pro Phe Tyr Ser Ser Pro Glu Leu Trp Ile Ser Ser Leu Pro Met  
115 120 125

40

Thr Asp Leu Asp Ile Lys Phe Gln Tyr Arg Gly Lys Glu Tyr Gly Gln  
130 135 140

45 Thr Met Thr Val Ser Asn Pro Gln Gly Cys Arg Leu Phe Tyr Gly Asp  
145 150 155 160

Leu Gly Pro Met Pro Asp Gln Glu Glu Leu Phe Gly Pro Val Xaa Leu  
165 170 175

50 Glu Gln Val Lys Phe Pro Gly Pro Glu His Ile Thr Asn Glu Lys Gln  
180 185 190

Lys Leu Phe Thr Ser Lys Leu Leu Asp Val Met Asp Arg Gly Leu Ile  
195 200 205

55

Leu Glu Val Ser Gly His Ala Ile Tyr Ala Ile Arg Leu Cys Gln Cys  
210 215 220

60 Lys Val Tyr Trp Ser Gly Pro Cys Ala Pro Ser Leu Val Ala Pro Asn  
225 230 235 240



Leu Ile Glu Arg Gln Lys Lys Val Lys Leu Phe Cys Leu Glu Thr Phe  
 245 250 255  
 5 Leu Ser Asp Leu Ile Ala His Gln Lys Gly Gln Ile Glu Lys Gln Pro  
 260 265 270  
 Pro Phe Glu Ile Tyr Leu Cys Phe Gly Glu Glu Trp Pro Asp Gly Lys  
 275 280 285  
 10 Pro Leu Glu Arg Lys Leu Ile Leu Val Gln Val Ile Pro Val Val Ala  
 290 295 300  
 Arg Met Ile Tyr Glu Met Phe Ser Gly Asp Phe Thr Arg Ser Phe Asp  
 15 305 310 315 320  
 Ser Gly Ser Val Arg Leu Gln Ile Ser Thr Pro Asp Ile Lys Asp Asn  
 325 330 335  
 20 Ile Val Ala Gln Leu Lys Gln Leu Tyr Arg Ile Leu Gln Thr Gln Glu  
 340 345 350  
 Ser Trp Gln Pro Met Gln Pro Thr Pro Ser Met Gln Leu Pro Pro Ala  
 355 360 365  
 25 Leu Pro Pro Gln Xaa  
 370

30

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

40 Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser  
 1 5 10 15  
 Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe  
 20 25 30  
 45 Trp Gly Phe Gly Arg Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr  
 35 40 45  
 Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser  
 50 55 60  
 55 His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln  
 65 70 75 80  
 Pro Asn Xaa

60

(2) INFORMATION FOR SEQ ID NO: 369:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala  
 1 5 10 15  
 10 Tyr Trp Thr Met Xaa  
 20

15

(2) INFORMATION FOR SEQ ID NO: 370:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Gly Ala Ser Ala Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro  
 1 5 10 15  
 25 Gly Ser Gly Lys Gly Thr Val Ser Ser Arg Ile Thr Thr His Phe Glu  
 20 25 30  
 30 Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Asp Asn Met Leu Arg  
 35 40 45  
 Gly Thr Glu Ile Gly Val Leu Ala Lys Ala Phe Ile Asp Gln Gly Lys  
 50 55 60  
 35 Leu Ile Pro Asp Asp Val Met Thr Arg Leu Ala Leu His Glu Leu Lys  
 65 70 75 80  
 Asn Leu Thr Gln Tyr Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu  
 85 90 95  
 40 Pro Gln Ala Glu Ala Leu Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile  
 100 105 110  
 Asn Leu Asn Val Pro Phe Glu Val Ile Lys Gln Arg Leu Thr Ala Arg  
 115 120 125  
 Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro  
 130 135 140  
 50 Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln  
 145 150 155 160  
 Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr  
 165 170 175  
 55 Glu Asp Gln Thr Lys Pro Val Leu Glu Tyr Tyr Gln Lys Lys Gly Val  
 180 185 190  
 60 Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val  
 195 200 205

Tyr Ala Phe Leu Gln Thr Lys Val Pro Gln Arg Ser Gln Lys Ala Ser  
 210 215 220

5 Val Thr Pro  
 225

10 (2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Phe Leu Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln  
 1 5 10 15

20

Leu Lys Ile Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu  
 20 25 30

25

Lys Ile Ile Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser  
 35 40 45

Trp Ala Ile Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn  
 50 55 60

30

Lys Thr Ala Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr Xaa  
 65 70 75

35 (2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ala Val Phe Pro Cys Cys Pro Phe Leu Thr Leu Met Leu Pro  
 1 5 10 15

45

Leu Leu Glu Cys Leu Val Gly Met Ile Met Cys Tyr Leu Gly Ile Ser  
 20 25 30

50

Phe Thr Asp Thr Arg Lys Thr Ala Gly Leu Lys Lys Lys Lys Lys Lys  
 35 40 45

Lys Xaa Xaa  
 50

55

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

60

577

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

5 Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser  
 1 5 10 15  
 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Ala Ser Tyr Leu Trp  
 20 25 30  
 10 Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Ser Trp Ala Cys  
 35 40 45  
 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu Xaa  
 15 50 55 60

(2) INFORMATION FOR SEQ ID NO: 374:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe  
 1 5 10 15  
 30 Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg  
 20 25 30  
 Ile Leu Phe Phe Ile Val Phe Xaa  
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 375:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Cys Ser Gly Gln Ser Gln Val Trp Lys Met Ala Leu Gln Ala Leu  
 1 5 10 15  
 50 Asp Ser Glu Thr Val Val Ile Leu Pro Asp Met His Leu Ile Leu Ser  
 20 25 30  
 Leu Arg Leu Ile His Asn Ala Arg Pro Cys Leu Xaa  
 35 40

55

(2) INFORMATION FOR SEQ ID NO: 376:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

5 Met Leu Ile Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp Pro Arg Asp  
 1 5 10 15  
 Glu Thr Tyr Lys Pro His Leu Glu Arg Glu Thr Pro Lys Pro Arg Arg  
 20 25 30  
 10 Lys Ser Gly Lys Val Lys Glu Glu Lys Glu Lys Lys Glu Ile Lys Val  
 35 40 45  
 Glu Val Glu Val Glu Val Lys Glu Glu Glu Asn Glu Ile Arg Glu Asp  
 15 50 55 60  
 Glu Glu Pro Pro Arg Lys Arg Gly Arg Arg Arg Lys Asp Asp Lys Ser  
 65 70 75 80  
 20 Pro Arg Leu Pro Lys Arg Arg Lys Lys Pro Pro Ile Gln Tyr Val Arg  
 85 90 95  
 Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His Pro Arg Tyr Leu  
 100 105 110  
 25 Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys Lys Tyr Val Cys  
 115 120 125  
 Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys Gln Leu Leu  
 130 135 140  
 Arg His Ala Lys His His Thr Asp Gln Arg Asp Tyr Ile Cys Glu Tyr  
 145 150 155 160  
 35 Cys Ala Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met  
 165 170 175  
 Ile His Thr Gly Glu Lys His Tyr Asn Val Arg Ser Val Asp Leu Leu  
 180 185 190  
 40 Val Asp Lys Arg His Leu Leu Ile Gly Thr Xaa  
 195 200

45

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

50

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

55 Met Leu Pro Arg Arg Thr Phe Tyr Phe Tyr Phe Ile Phe Ile Phe Phe  
 1 5 10 15  
 Leu Ala Ser Phe Trp Gly Phe Thr Leu Arg Ala Ser Phe  
 20 25

60

## (2) INFORMATION FOR SEQ ID NO: 378:

## (i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

10 Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu Met  
     1                    5                    10                    15  
  
 Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val Leu  
                     20                    25                    30  
 15 Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu Trp  
                     35                    40                    45  
  
 Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg Met  
 20                    50                    55                    60  
  
 Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val Gln  
                     65                    70                    75                    80  
  
 25 Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu Asn  
                     85                    90                    95  
  
 Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met Pro Ser Phe  
                     100                    105                    110  
 30 Phe Ser Cys His Leu Phe Cys Thr Leu Arg Trp Lys Tyr Phe Glu Val  
                     115                    120                    125  
  
 Phe Tyr Asn His Lys Phe Leu Xaa  
 35                    130                    135

## (2) INFORMATION FOR SEQ ID NO: 379:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Ala Trp Arg Arg Arg Glu Pro Ala Ser Gly Leu Ala Ala Cys Trp  
     1                    5                    10                    15  
  
 50 Leu Trp Arg Cys Ser Pro Trp Pro Cys Ala Cys Pro Gly Pro Gly Ala  
                     20                    25                    30  
  
 Gly Leu Ser Ser Gly Ser Arg Pro Trp  
                     35                    40  
 55

## (2) INFORMATION FOR SEQ ID NO: 380:

60

## (i) SEQUENCE CHARACTERISTICS:

580

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

5 Met Glu Phe Leu Lys Val Ala Arg Arg Asn Lys Arg Glu Gln Leu Glu  
 1 5 10 15  
 10 Gln Ile Gln Lys Glu Leu Ser Val Leu Glu Glu Asp Ile Lys Arg Val  
 20 25 30  
 Glu Glu Met Ser Gly Leu Tyr Ser Pro Val Ser Glu Asp Ser Thr Val  
 35 40 45  
 15 Pro Gln Phe Glu Ala Pro Ser Pro Ser His Ser Ser Ile Ile Asp Ser  
 50 55 60  
 Thr Glu Tyr Ser Gln Pro Pro Gly Phe Ser Gly Ser Ser Gln Thr Lys  
 65 70 75 80  
 20 Lys Gln Pro Trp Tyr Asn Ser Thr Leu Ala Ser Arg Arg Lys Arg Leu  
 85 90 95  
 Thr Ala His Phe Glu Asp Leu Glu Gln Cys Tyr Phe Ser Thr Arg Met  
 100 105 110  
 Ser Arg Ile Ser Asp Asp Ser Arg Thr Ala Ser Gln Leu Asp Glu Phe  
 115 120 125  
 30 Gln Glu Cys Leu Ser Lys Phe Thr Arg Tyr Asn Ser Val Arg Pro Leu  
 130 135 140  
 Ala Thr Leu Ser Tyr Ala Ser Asp Leu Tyr Asn Gly Ser Ser Ile Val  
 145 150 155 160  
 35 Ser Ser Ile Glu Phe Asp Arg Asp Cys Asp Tyr Phe Ala Ile Ala Gly  
 165 170 175  
 Val Thr Lys Lys Ile Lys Val Tyr Glu Tyr Asp Thr Val Ile Gln Asp  
 180 185 190  
 Ala Val Asp Ile His Tyr Pro Glu Asn Glu Met Thr Cys Asn Ser Lys  
 195 200 205  
 45 Ile Ser Cys Ile Ser Trp Ser Ser Tyr His Lys Asn Leu Leu Ala Ser  
 210 215 220  
 Ser Asp Tyr Glu Gly Thr Val Ile Leu Trp Asp Gly Phe Thr Gly Gln  
 225 230 235 240  
 50 Arg Ser Lys Val Tyr Gln Glu His Glu Lys Arg Cys Trp Ser Val Asp  
 245 250 255  
 Phe Asn Leu Met Asp Pro Lys Leu Leu Ala Ser Gly Ser Asp Asp Ala  
 260 265 270  
 Lys Val Lys Leu Trp Ser Thr Asn Leu Asp Asn Ser Val Ala Ser Ile  
 275 280 285  
 60 Glu Ala Lys Ala Asn Val Cys Cys Val Lys Phe Ser Pro Ser Ser Arg

581.

290                      295                      300

Tyr His Leu Ala Phe Gly Cys Ala Asp His Cys Val His Tyr Tyr Asp  
305                      310                      315                      320

5 Leu Arg Asn Thr Lys Gln Pro Ile Met Val Phe Lys Gly His Arg Lys  
                    325                      330                      335

10 Ala Val Ser Tyr Ala Lys Phe Val Ser Gly Glu Glu Ile Val Ser Ala  
                    340                      345                      350

Ser Thr Asp Ser Gln Leu Lys Leu Trp Asn Val Gly Lys Pro Tyr Cys  
355                      360                      365

15 Leu Arg Ser Phe Lys Gly His Ile Asn Glu Lys Asn Phe Val Gly Leu  
370                      375                      380

Ala Ser Asn Gly Asp Tyr Ile Ala Cys Gly Ser Glu Asn Asn Ser Leu  
385                      390                      395                      400

20 Tyr Leu Tyr Tyr Lys Gly Leu Ser Lys Thr Leu Leu Thr Phe Lys Phe  
                    405                      410                      415

25 Asp Thr Val Lys Ser Val Leu Asp Lys Asp Arg Lys Glu Asp Asp Thr  
420                      425                      430

Asn Glu Phe Val Ser Ala Val Cys Trp Arg Ala Leu Pro Asp Gly Glu  
435                      440                      445

30 Ser Asn Val Leu Ile Ala Ala Asn Ser Gln Gly Thr Ile Lys Val Leu  
450                      455                      460

Glu Leu Val Xaa  
465

35

(2) INFORMATION FOR SEQ ID NO: 381:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

45

Met Arg Lys Glu Asp Gly Phe Trp Phe Phe Phe Phe Leu Phe Phe Phe  
1                      5                      10                      15

50

Val Val Gly Ser Lys Phe Val Asn Gly Asn Lys Leu Val  
20                      25

55

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:



Met Pro Leu Ala Pro Tyr Cys Asp Leu Leu Val Ala Leu Ser Phe Ala  
1 5 10 15

5 Leu Val Leu Glu Ser Pro Val Asp Ser Ser Asp Phe Thr  
20 25

10 (2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Asn Ser Leu Val Ser Trp Gln Leu Leu Leu Phe Leu Cys Ala Thr  
1 5 10 15

20 His Phe Gly Glu Pro Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg  
20 25 30

25 Pro Thr Gly Gln Gln Leu Glu Ser Leu Gly Leu Leu Ala Pro Gly Glu  
35 40 45

Gln Ser Leu Pro Cys Thr Glu Arg Lys Pro Ala Ala Thr Ala Arg Leu  
50 55 60

30 Ser Arg Arg Gly Thr Ser Leu Ser Pro Pro Pro Glu Ser Ser Gly Ser  
65 70 75 80

Pro Gln Gln Pro Gly Leu Ser Ala Pro His Ser Arg Gln Ile Pro Ala  
85 90 95

35 Pro Gln Gly Ala Val Leu Val Gln Arg Glu Lys Asp Leu Pro Asn Tyr  
100 105 110

40 Asn Trp Asn Ser Phe Gly Leu Arg Phe Gly Lys Arg Glu Ala Ala Pro  
115 120 125

Gly Asn His Gly Arg Ser Ala Gly Arg Gly  
130 135

45

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

55 Met Ser Cys Phe Ile Asp Ser Xaa Asp Ser Lys Ile Leu His Leu Leu  
1 5 10 15

Val Val Ser Phe Ile Cys Xaa Leu Phe Leu Leu Ile Leu Thr His Gly  
20 25 30

60

Ile Leu Ile Leu Arg Xaa Phe Phe Ser Val Xaa Xaa His Ser Leu Lys  
 35 40 45  
 5 Asn Asn Leu Glu Glu Tyr Leu Ile Leu Met Asn Lys Ala Leu Leu Thr  
 50 55 60  
 Arg Glu Asp Phe Phe Val Leu Pro Xaa Ala  
 65 70

10

(2) INFORMATION FOR SEQ ID NO: 385:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 521 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

20 Met Ser Ala Gly Glu Val Glu Arg Leu Val Ser Glu Leu Ser Gly Gly  
 1 5 10 15  
 Thr Gly Gly Asp Glu Glu Glu Glu Trp Leu Tyr Gly Asp Glu Asn Glu  
 20 25 30  
 25 Val Glu Arg Pro Glu Glu Glu Asn Ala Ser Ala Asn Pro Pro Ser Gly  
 35 40 45  
 30 Ile Glu Asp Glu Thr Ala Glu Asn Gly Val Pro Lys Pro Lys Val Thr  
 50 55 60  
 Glu Thr Glu Asp Asp Ser Asp Ser Asp Ser Asp Asp Asp Glu Asp Asp  
 65 70 75 80  
 35 Val His Val Thr Ile Gly Asp Ile Lys Thr Gly Ala Pro Gln Tyr Gly  
 85 90 95  
 Ser Tyr Gly Thr Ala Pro Val Asn Leu Asn Ile Lys Thr Gly Gly Arg  
 100 105 110  
 40 Val Tyr Gly Thr Thr Gly Thr Lys Val Lys Gly Val Asp Leu Asp Ala  
 115 120 125  
 Pro Gly Ser Ile Asn Gly Val Pro Leu Leu Glu Val Asp Leu Asp Ser  
 130 135 140  
 Phe Glu Asp Lys Pro Trp Arg Lys Pro Gly Ala Asp Leu Ser Asp Tyr  
 145 150 155 160  
 50 Phe Asn Tyr Gly Phe Asn Glu Asp Thr Trp Lys Ala Tyr Cys Glu Lys  
 165 170 175  
 Gln Lys Arg Ile Arg Met Gly Leu Glu Val Ile Pro Val Thr Ser Thr  
 180 185 190  
 55 Thr Asn Lys Ile Thr Val Gln Gln Gly Arg Thr Gly Asn Ser Glu Lys  
 195 200 205  
 Glu Thr Ala Leu Pro Ser Thr Lys Ala Glu Phe Thr Ser Pro Pro Ser  
 210 215 220  
 60

Leu Phe Lys Thr Gly Leu Pro Pro Ser Arg Arg Leu Pro Gly Ala Ile  
 225 230 235 240  
 5 Asp Val Ile Gly Gln Thr Ile Thr Ile Ser Arg Val Glu Gly Arg Arg  
 245 250 255  
 Arg Ala Asn Glu Asn Ser Asn Ile Gln Val Leu Ser Glu Arg Ser Ala  
 260 265 270  
 10 Thr Glu Val Asp Asn Asn Phe Ser Lys Pro Pro Pro Phe Phe Pro Pro  
 275 280 285  
 Gly Ala Pro Pro Thr His Leu Pro Pro Pro Pro Phe Leu Pro Pro Pro  
 15 290 295 300  
 Pro Thr Val Ser Thr Ala Pro Pro Leu Ile Pro Pro Pro Gly Phe Pro  
 305 310 315 320  
 20 Pro Pro Pro Gly Ala Pro Pro Pro Ser Leu Ile Pro Thr Ile Glu Ser  
 325 330 335  
 Gly His Ser Ser Gly Tyr Asp Ser Arg Ser Ala Arg Ala Phe Pro Tyr  
 25 340 345 350  
 Gly Asn Val Ala Phe Pro His Leu Pro Gly Ser Ala Pro Ser Trp Pro  
 355 360 365  
 Ser Leu Val Asp Thr Ser Lys Gln Trp Asp Tyr Tyr Ala Arg Arg Glu  
 30 370 375 380  
 Lys Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp  
 385 390 395 400  
 35 Arg Asp Arg Glu Arg Glu Arg Thr Arg Glu Arg Glu Arg Glu Arg Asp  
 405 410 415  
 His Ser Pro Thr Pro Ser Val Phe Asn Ser Asp Glu Glu Arg Tyr Arg  
 420 425 430  
 40 Tyr Arg Glu Tyr Ala Glu Arg Gly Tyr Glu Arg His Arg Ala Ser Arg  
 435 440 445  
 Glu Lys Glu Glu Arg His Arg Glu Arg Arg His Arg Glu Lys Glu Glu  
 45 450 455 460  
 Thr Arg His Lys Ser Ser Arg Ser Asn Ser Arg Arg Arg His Glu Ser  
 465 470 475 480  
 50 Glu Glu Gly Asp Ser His Arg Arg His Lys His Lys Lys Ser Lys Arg  
 485 490 495  
 Ser Lys Glu Gly Lys Glu Ala Gly Ser Glu Pro Ala Pro Glu Gln Glu  
 500 505 510  
 55 Ser Thr Glu Ala Thr Pro Ala Glu Xaa  
 515 520  
 60

585

## (2) INFORMATION FOR SEQ ID NO: 386:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

5 Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu  
 10 1 5 10 15  
 Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val  
 20 25 30  
 15 Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu  
 35 40 45  
 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala  
 50 55 60  
 20 Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr  
 65 70 75 80  
 Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu  
 25 85 90 95  
 Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr  
 100 105 110  
 30 Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly  
 115 120 125  
 Val Arg Val Phe Gly Ile Asn Lys Tyr  
 130 135  
 35

## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

40 Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu  
 1 5 10 15  
 45 Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg  
 20 25 30  
 Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe  
 35 40 45  
 55 Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys  
 50 55 60  
 Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe  
 65 70 75 80  
 60

586

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu  
85 90 95

5 Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr Leu  
100 105 110

Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser Pro  
115 120 125

10 Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe Trp  
130 135 140

Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr Leu  
145 150 155 160

15 Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val Asp  
165 170 175

Gly Glu Glu Leu Gln Met Glu Pro Val Xaa  
20 180 185

(2) INFORMATION FOR SEQ ID NO: 388:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met

1

35

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

45

Met Leu Ser Ile Phe Tyr Phe Ala Ile Pro Val Gly Ser Gly Leu Gly  
1 5 10 15

Tyr Ile Ala Gly Ser Lys Val Lys Asp Met Ala Gly Asp Trp His Trp  
20 25 30

50

Ala Leu Arg Val Thr Pro Gly Leu Gly Val Val Ala Val Leu Leu Leu  
35 40 45

55

Phe Leu Val Val Arg Glu Pro Pro Arg Gly Ala Val Glu Arg His Ser  
50 55 60

Asp Leu Pro Pro Leu Asn Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala  
65 70 75 80

60

Leu Ala Arg Asn Pro Ser Phe Val Leu Ser Ser Leu Gly Phe Thr Ala

587

85                      90                      95  
 Val Ala Phe Val Thr Gly Ser Leu Ala Leu Trp Ala Pro Ala Phe Leu  
                          100                      105                      110  
 5    Leu Arg Ser Arg Val Val Leu Gly Glu Thr Pro Pro Cys Leu Pro Gly  
                          115                      120                      125  
 10    Asp Ser Cys Ser Ser Ser Asp Ser Leu Ile Phe Gly Leu Ile Thr Cys  
                          130                      135                      140  
 Leu Thr Gly Val Leu Gly Val Gly Leu Gly Val Glu Ile Ser Arg Arg  
 145                                   150                      155                      160  
 15    Leu Arg His Ser Asn Pro Arg Ala Asp Pro Leu Val Cys Ala Thr Gly  
                                  165                      170                      175  
 Leu Leu Gly Ser Ala Pro Phe Leu Phe Leu Ser Leu Ala Cys Ala Arg  
 180                                   185                      190  
 20    Gly Ser Ile Val Ala Thr Tyr Ile Phe Ile Phe Ile Gly Glu Thr Leu  
                          195                      200                      205  
 Leu Ser Met Asn Trp Ala Ile Val Ala Asp Ile Leu Leu Tyr Val Val  
 210                                   215                      220  
 Ile Pro Thr Arg Arg Ser Thr Ala Glu Ala Phe Gln Ile Val Leu Ser  
 225                                   230                      235                      240  
 30    His Leu Leu Gly Asp Ala Gly Ser Pro Tyr Leu Ile Gly Leu Ile Ser  
                                  245                      250                      255  
 Asp Arg Leu Arg Arg Asn Trp Pro Pro Ser Phe Leu Ser Glu Phe Arg  
 260                                   265                      270  
 35    Ala Leu Gln Phe Ser Leu Met Leu Cys Ala Phe Val Gly Ala Leu Gly  
                          275                      280                      285  
 Gly Ala Leu Pro Gly His Arg His Leu His Xaa  
 290                                   295  
 40

(2) INFORMATION FOR SEQ ID NO: 390:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Gly Pro Gln Gly Trp Val Arg Pro Leu Lys Thr Ala Pro Lys Leu  
 1                      5                      10                      15

55

Gly Glu Ala Ile Arg Leu Ile Leu Phe Leu Asn Phe Val Lys Gln Cys  
 20                      25                      30

Ile Ala Ser Val Asn Leu Cys Ile Leu Arg Leu Asn Ile Thr Pro Leu  
 35                      40                      45

60

Leu

5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

15 Met Tyr Val Asn Tyr Gly Thr Arg Asn Tyr Ser Thr Glu Gly Pro Ala  
1 5 10 15

Ala Leu Leu Asp Gln Ala Lys Leu Ser Leu Leu Val Trp Val Leu Cys  
20 25 30

20 Phe Val Leu Leu Phe Val Cys Phe Cys Gly Leu Ser Tyr Val Val Ile  
35 40 45

Ala Gln Val Pro Val Gly Leu Leu Cys Ile Thr Glu Xaa  
50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 392:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

35

Met Leu Trp Phe Ala Asn Phe Phe Thr Tyr Leu Phe Leu Ser Gln Ser  
1 5 10 15

40 Val Ala Phe Val His Ile Ser His Ile Gly Val Arg Gln Val Asn Thr  
20 25 30

Asn Cys Tyr Phe Ser Arg Lys Ser Tyr Cys Tyr Gly Ile Leu Asn Pro  
35 40 45

45 Ile Asn Cys Ile Lys Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys  
50 55 60

Lys Lys Lys Lys Ile Pro Ala Gly Arg Xaa Leu Phe Pro Phe Gly  
65 70 75

50

(2) INFORMATION FOR SEQ ID NO: 393:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

60

589

Met Pro Gly Ala Phe Ser Glu Thr Val Ile Asn Asp Leu Leu Ser Leu  
 1 5 10 15  
 Phe Leu Val Leu Pro Ala Glu Leu Ser Tyr Ser Thr Leu Ser Gly Val  
 5 20 25 30  
 Tyr Arg Asn Ala  
 35

10

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:  
 15 (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

20 Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu  
 1 5 10 15  
 Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser  
 20 25 30  
 25 Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu  
 35 40 45  
 30 Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro  
 50 55 60  
 Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro  
 65 70 75 80  
 35 Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr  
 85 90 95  
 Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu  
 100 105 110  
 40 Leu Asp Arg Arg Ser Glu Ser Cys Ser Met Leu Pro Trp Xaa Ala Gln  
 115 120 125  
 45 Leu Leu Asp Arg Thr Ile Gly Pro Leu Tyr Leu Leu Phe Val Gln Phe  
 130 135 140  
 Ser Pro Ala Phe Ser Arg Thr Ser Pro Trp Arg Ser Pro Lys Asn Phe  
 145 150 155 160  
 50 Arg Arg Leu Tyr Pro Pro Cys Thr Thr Ser Gly Cys Ala Ala Arg Trp  
 165 170 175  
 Xaa Phe Ser Xaa  
 180

55

(2) INFORMATION FOR SEQ ID NO: 395:

60 (i) SEQUENCE CHARACTERISTICS:



590

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

5

Met Pro Thr Pro Cys Thr Ser Leu Pro Ser Cys Cys Gln His Arg Ser  
 1 5 10 15

10

Ile Thr Met Thr Leu  
 20

15

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Pro Leu Phe Ile Pro Leu Ile Phe Phe Leu Ser Leu Leu His Cys  
 1 5 10 15

25

Gln Ser Lys His Pro Ile Gln Met Ser Leu Cys Met Cys Val Asn Ile  
 20 25 30

30

Ser Leu Val Trp Ser Pro Val Arg Trp Ile Phe Gly Ser Lys Gly Leu  
 35 40 45

Phe Ser Val His Leu Gln Ser Ser Gln Arg Pro Ser  
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

45

Met Ala Gly Pro Arg Pro Xaa Trp Arg Asp Gln Leu Leu Phe Met Ser  
 1 5 10 15

Ile Ile Val Leu Val Ile Val Val Ile Cys Leu Met Leu Tyr Ala Leu  
 20 25 30

50

Leu Trp Glu Ala Gly Asn Leu Thr Asp Leu Pro Asn Leu Arg Ile Gly  
 35 40 45

Phe Tyr Asn Phe Cys Leu Trp Asn Glu Asp Thr Ser Thr Leu Gln Cys  
 50 55 60

55

His Gln Phe Pro Glu Leu Glu Ala Leu Gly Val Pro Arg Val Gly Leu  
 65 70 75 80

60

Gly Leu Ala Arg Leu Gly Val Tyr Gly Ser Leu Val Leu Thr Leu Phe  
 85 90 95

Ala Pro Gln Pro Leu Leu Leu Ala Gln Cys Asn Xaa Asp Glu Arg Ala  
100 105 110

5 Trp Arg Leu Ala Val Gly Phe Leu Ala Val Ser Ser Val Leu Leu Ala  
115 120 125

Gly Gly Leu Gly Leu Phe Leu Ser Tyr Val Trp Asn Gly Ser Xaa Ser  
130 135 140

10 Pro Ser Arg Gly Leu Gly Phe Xaa  
145 150

15 (2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

25 Met Ser Asp Gly Phe Asp Arg Ala Pro Gly Ala Gly Arg Gly Arg Xaa  
1 5 10 15

Arg Gly Leu Gly Arg Gly Gly Gly Gly Pro Xaa Gly Gly Gly Phe Pro  
20 25 30

30 Xaa Gly Xaa Xaa Pro Ala Glu Arg Xaa Arg His Gln Pro Pro Gln Pro  
35 40 45

Lys Ala Pro Gly Phe Leu Gln Pro Xaa Pro Leu Arg Gln Pro Arg Thr  
50 55 60

35 Thr Pro Pro Pro Gly Ala Gln Cys Glu Val Pro Ala Ser Pro Gln Arg  
65 70 75 80

40 Pro Ser Arg Pro Gly Ala Leu Pro Glu Gln Thr Arg Pro Leu Arg Ala  
85 90 95

Pro Pro Ser Ser Gln Asp Lys Ile Pro Gln Gln Asn Ser Glu Ser Ala  
100 105 110

45 Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu  
115 120 125

Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr  
130 135 140

50 Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu  
145 150 155 160

55 Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe  
165 170 175

Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr  
180 185 190

60 Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala

592

	195	200	205
	Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr		
	210	215	220
5	Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln		
	225	230	235 240
10	Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala		
	245	250	255
	Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu		
	260	265	270
15	Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly		
	275	280	285
	Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu		
20	290	295	300
	Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val		
	305	310	315 320
25	Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu		
	325	330	335
	Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val		
	340	345	350
30	Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys		
	355	360	365
	Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser		
35	370	375	380
	Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn		
	385	390	395 400
40	Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp		
	405	410	415
	Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe		
	420	425	430
45	Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp		
	435	440	445
	Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu		
50	450	455	460
	Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln Xaa		
	465	470	475 480

55

(2) INFORMATION FOR SEQ ID NO: 399:

60

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Glu Pro Lys Thr Ile Thr Asp Ala Leu Ala Ser Ser Ile Ile Lys  
 1 5 10 15  
 10 Ser Val Leu Pro Asn Phe Leu Pro Tyr Asn Val Met Leu Tyr Ser Asp  
 20 25 30  
 Ala Pro Val Ser Glu Leu Ser Leu Glu Leu Leu Leu Gln Val Val  
 35 40 45  
 15 Leu Pro Ala Leu Leu Glu Gln Gly His Thr Arg Gln Trp Leu Lys Gly  
 50 55 60  
 20 Leu Val Arg Ala Trp Thr Val Thr Ala Gly Tyr Leu Leu Asp Leu His  
 65 70 75 80  
 Ser Tyr Leu Leu Gly Asp Gln Glu Glu Asn Glu Asn Ser Ala Asn Gln  
 85 90 95  
 25 Gln Val Asn Asn Asn Gln His Ala Arg Asn Asn Asn Ala Ile Pro Val  
 100 105 110  
 Val Gly Glu Gly Leu His Ala Ala His Gln Ala Ile Leu Gln Gln Gly  
 115 120 125  
 30 Gly Pro Val Gly Phe Gln Xaa Tyr Arg Arg Pro Leu Asn Phe Pro Leu  
 130 135 140  
 35 Arg Ile Phe Leu Leu Ile Val Phe Met Cys Ile Thr Leu Leu Ile Ala  
 145 150 155 160  
 Ser Leu Ile Cys Leu Thr Leu Pro Val Phe Ala Gly Arg Trp Leu Met  
 165 170 175  
 40 Ser Phe Trp Thr Gly Thr Ala Lys Ile His Glu Leu Tyr Thr Ala Ala  
 180 185 190  
 Cys Gly Leu Tyr Val Cys Trp Leu Thr Ile Arg Ala Val Thr Val Met  
 195 200 205  
 45 Val Ala Trp Met Pro Gln Gly Arg Arg Val Ile Phe Gln Lys Val Lys  
 210 215 220  
 Glu Trp Ser Leu Met Ile Met Lys Thr Leu Ile Val Ala Val Leu Leu  
 225 230 235 240  
 Ala Gly Val Val Pro Leu Leu Leu Gly Leu Leu Phe Glu Leu Val Ile  
 245 250 255  
 55 Val Ala Pro Leu Arg Val Pro Leu Asp Gln Thr Pro Leu Phe Tyr Pro  
 260 265 270  
 Trp Gln Asp Trp Ala Leu Gly Val Leu His Ala Lys Ile Ile Ala Ala  
 275 280 285  
 60

594

Ile Thr Leu Met Gly Pro Gln Trp Trp Leu Lys Thr Val Ile Glu Gln  
 290 295 300

5 Val Tyr Ala Asn Gly Ile Arg Asn Ile Asp Leu His Tyr Ile Val Arg  
 305 310 315 320

Lys Leu Ala Ala Pro Val Ile Ser Val Leu Leu Ser Leu Cys Val  
 325 330 335

10 Pro Tyr Val Ile Ala Ser Gly Val Val Pro Leu Leu Gly Val Thr Ala  
 340 345 350

Glu Met Gln Asn Leu Val His Arg Arg Ile Tyr Pro Phe Leu Leu Met  
 355 360 365

15 Val Val Val Leu Met Ala Ile Leu Ser Phe Gln Val Arg Gln Phe Lys  
 370 375 380

Arg Leu Tyr Glu His Ile Lys Asn Asp Lys Tyr Leu Val Gly Gln Arg  
 20 385 390 395 400

Leu Val Asn Tyr Glu Arg Lys Ser Gly Lys Gln Gly Ser Ser Pro Pro  
 405 410 415

25 Pro Pro Gln Ser Ser Gln Glu  
 420

30 (2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met  
 1 5 10 15

40 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr  
 20 25 30

Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala  
 35 40 45

45 Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro  
 50 55 60

50 Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu Xaa  
 65 70 75

55 (2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

5 Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser  
 1 5 10 15  
 His Cys Trp Gly Leu Pro Leu His Val Ala Pro Leu Cys Arg Gly His  
 20 25 30  
 10 Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala Trp  
 35 40 45  
 Asn Arg Asn Leu Ala Asn Gln Arg His Phe Phe Cys Pro Ser Ile Phe  
 50 55 60  
 15 His Thr Cys Pro Thr Val Leu Phe Phe Xaa  
 65 70

## 20 (2) INFORMATION FOR SEQ ID NO: 402:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

30 Ala Arg Thr Ile Leu Val Leu Tyr Leu Ser Leu Gln Arg Leu Glu Asn  
 1 5 10 15  
 Leu Ala Tyr His  
 20

## 35 (2) INFORMATION FOR SEQ ID NO: 403:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 87 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

45 Met Pro Leu Pro Ser Val Pro Ile Leu Gly Ile Phe Ser Phe Leu Ile  
 1 5 10 15  
 Pro Ser Ser Gln Gly Val Ser Tyr Thr Lys Leu Pro Ile Ser Ser Pro  
 20 25 30  
 50 Gln Tyr Ser Pro Phe Val Asn Asp His Phe Ser Phe Leu Asn Pro Phe  
 35 40 45  
 Pro Val Gln Ile His Thr Gly Phe Ala Arg Val Gly Ser Tyr Met Gln  
 50 55 60  
 55 Met Pro Leu Val His Leu Cys Leu Leu Gln Thr Ser Leu Met Lys Asn  
 65 70 75 80  
 60 Ser Gly Val Gln Gln Gly Ser  
 85

## (2) INFORMATION FOR SEQ ID NO: 404:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile Ile  
 1 5 10 15

15

Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala Val  
 20 25 30

20

Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile Thr  
 35 40 45

Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val Tyr  
 50 55 60

25

Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg Asp  
 65 70 75 80

Gln Thr Lys Ser Ile Val Glu Lys Ile Pro Ser Lys  
 85 90

30

## (2) INFORMATION FOR SEQ ID NO: 405:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

40

Met Ala Cys Ser Cys Leu Met Ile Gln Ser Phe Ser Thr Ser Ala Leu  
 1 5 10 15

Val Leu Phe Tyr Gly  
 20

45

## (2) INFORMATION FOR SEQ ID NO: 406:

50

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

55

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu  
 1 5 10 15

60

Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val  
 20 25 30

Ser Gly Phe Pro Ala Phe Pro Lys Pro Ser Pro Thr Tyr Leu Arg Thr  
 35 40 45  
 5 Ser Ala Glu Gln Thr Leu Pro Leu Leu Leu Pro His Leu His Gly Leu  
 50 55 60  
 Cys Leu His Gln Pro Leu His Leu Gly Phe Thr Ala Cys Leu Gly Ser  
 65 70 75 80  
 10 Ala His Ile Leu Gly Gly Gln Pro Ala Leu Pro Ala Val Pro Glu Pro  
 85 90 95  
 Tyr Ala Gly His Cys Gln Arg Pro Leu Ala Gly Thr Pro His His Ser  
 15 100 105 110  
 Cys His Val Gly Pro Ala Asn Arg Gly Arg Arg Ser Glu Ala Trp Val  
 115 120 125  
 20 Gly Arg Tyr Gln Ala Ala Asn Arg Phe Pro Ile Leu Asn Ala Xaa Cys  
 130 135 140  
 Glu Arg Arg Thr Pro Ser Thr Val Leu Ser Ala Arg Ile Ser Ser Ala  
 145 150 155 160  
 25 Thr Met Gly Cys Pro Leu Phe Ala Ile Trp Ala Ala Ser Xaa  
 165 170

30

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 64 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

40

Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu  
 1 5 10 15

Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His  
 20 25 30

45

Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys  
 35 40 45

Thr Glu Gly Ile Pro Cys Gln Arg Tyr Gln Asn Gly Leu His Ile Xaa  
 50 55 60

50

55

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

60

- (A) LENGTH: 280 amino acids  
 (B) TYPE: amino acid



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

5 Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp  
 1 5 10 15  
 Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr  
 20 25 30  
 10 Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg  
 35 40 45  
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val  
 50 55 60  
 15 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe  
 65 70 75 80  
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val  
 85 90 95  
 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp  
 100 105 110  
 25 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe  
 115 120 125  
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His  
 130 135 140  
 30 His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro  
 145 150 155 160  
 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val  
 165 170 175  
 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln  
 180 185 190  
 40 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln  
 195 200 205  
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser  
 210 215 220  
 45 Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly  
 225 230 235 240  
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr  
 245 250 255  
 50 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly  
 260 265 270  
 55 Ile Ala Lys Val Lys Ala Asn Xaa  
 275 280

60 (2) INFORMATION FOR SEQ ID NO: 409:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

5 Met Xaa Leu Trp Pro Gln Thr Cys Ser Gly Lys Phe Asp Gly Thr Leu  
 1 5 10 15  
 10 Ala Phe Ser Ile His Xaa Leu Ala Val Ile Leu Gly Asp Gln Leu Thr  
 20 25 30  
 15 Ala Ala Asp Leu Val Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp  
 35 40 45  
 Glu Val Arg Ile Gly Val Leu Lys His Leu His Asp Phe Leu Lys Leu  
 50 55 60  
 20 Leu His Ile Asp Lys Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe  
 65 70 75 80  
 Leu Val Thr Asp Asn Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala  
 85 90 95  
 25 Glu Gln Leu Ile Leu Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr  
 100 105 110  
 30 Asp Tyr Leu Arg Pro Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser  
 115 120 125  
 Ser Val Arg Trp Ile Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys  
 130 135 140  
 35 Leu His Ala Ala Thr Pro Pro Thr Phe Gly Val Asp Leu Ile Asn Glu  
 145 150 155 160  
 Leu Val Glu Asn Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala  
 165 170 175  
 40 Phe Val Phe Val Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met  
 180 185 190  
 45 Asp Gln Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn  
 195 200 205  
 Asp Arg Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln  
 210 215 220  
 50 Thr Leu Leu Glu Lys Asp Tyr Phe Leu Ala Ser Ala Ser Cys His Gln  
 225 230 235 240  
 Glu Ala Val Glu Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser  
 245 250 255  
 55 Asp Val Lys Tyr Phe Ala Ser Ile His Pro Ala Ser Thr Lys Ile Ser  
 260 265 270  
 60 Glu Asp Ala Met Ser Thr Ala Ser Ser Thr Tyr Xaa  
 275 280

(2) INFORMATION FOR SEQ ID NO: 410:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Leu Phe Leu Phe Phe Val Ile Ile Phe Leu Phe Val Phe Leu Ile  
1 5 10 15

15

Leu Ile Ile Gln Phe Ser Lys Pro Leu Thr Asn Pro His Pro Pro Ala  
20 25 30

Gly Xaa Ser Asp Arg Arg Arg Arg Tyr Ser Ser Tyr Arg Ser His Asp  
35 40 45

20

His Tyr Gln Arg Gln Arg Val Leu Gln Lys Glu Arg Ala Ile Glu Glu  
50 55 60

25

Arg Arg Val Val Phe Ile Gly Lys Ile Pro Gly Arg Met Thr Arg Ser  
65 70 75 80

Glu Leu Lys Gln Arg Phe Ser Val Phe Gly Glu Ile Glu Glu Cys Thr  
85 90 95

30

Ile His Phe Arg Val Gln Gly Asp Asn Tyr Gly Phe Val Thr Tyr Arg  
100 105 110

Tyr Ala Glu Glu Ala Phe Ala Ala Ile Glu Ser Gly His Lys Leu Arg  
115 120 125

35

Gln Ala Asp Glu Gln Pro Phe Asp Leu Cys Phe Gly Gly Arg Arg Xaa  
130 135 140

40

Xaa Cys Lys Arg Ser Tyr Ser Asp Leu Asp Ser Asn Arg Glu Asp Phe  
145 150 155 160

Asp Pro Ala Pro Val Lys Ser Lys Phe Asp Ser Leu Asp Phe Asp Thr  
165 170 175

45

Leu Leu Lys Gln Ala Gln Lys Asn Leu Arg Arg  
180 185

50

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Lys Leu Pro Gly Lys Phe Arg Arg Ala His Gln Gly Asn Leu Glu  
1 5 10 15

60

601

Ser Gln Leu Thr Ser Glu Ser Tyr Tyr Lys Glu Thr Leu Ser Val Pro  
 20 25 30  
 5 Thr Val Glu His Ile Ile Gln Glu Leu Lys Asp Ile Phe Ser Glu Gln  
 35 40 45  
 His Leu Lys Ala Leu Lys Cys Leu Ser Leu Val Pro Ser Val Met Gly  
 50 55 60  
 10 Gln Leu Lys Phe Asn Thr Ser Glu Glu His His Ala Asp Met Tyr Arg  
 65 70 75 80  
 Ser Asp Leu Pro Asn Pro Asp Thr Leu Ser Ala Glu Leu His Cys Trp  
 85 90 95  
 15 Arg Ile Lys Trp Lys His Arg Gly Lys Asp Ile Glu Leu Pro Ser Thr  
 100 105 110  
 Ile Tyr Glu Ala Leu His Leu Pro Asp Ile Lys Phe Phe Pro Asn Val  
 115 120 125  
 Tyr Ala Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu  
 130 135 140  
 25 Asn Glu Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg  
 145 150 155 160  
 Asn Thr Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile  
 165 170 175  
 30 Asn Phe Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile  
 180 185 190  
 Lys Leu Tyr Thr Xaa Xaa Ser Xaa Leu Xaa Thr Xaa Xaa Ser Xaa Xaa  
 195 200 205  
 35 Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa  
 210 215 220  
 40 Asp Xaa Xaa Xaa Arg Glu Lys Ala Val Arg Cys Met Xaa  
 225 230 235

45 (2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Lys Pro Met Ala Val Val Ala Ser Thr Val Leu Gly Leu Val Gln  
 1 5 10 15  
 55 Asn Met Arg Ala Phe Gly Gly Ile Leu Val Val Val Tyr Tyr Val Phe  
 20 25 30  
 Ala Ile Ile Gly Ile Asn Leu Phe Arg Gly Val Ile Val Ala Leu Pro  
 35 40 45

Gly Asn Ser Ser Leu Ala Pro Ala Asn Gly Ser Ala Pro Cys Gly Ser  
 50 55 60  
 5 Phe Glu Gln Leu Glu Tyr Trp Ala Asn Asn Phe Asp Asp Phe Ala Ala  
 65 70 75 80  
 Ala Leu Val Thr Leu Trp Asn Leu Met Val Val Asn Asn Trp Gln Val  
 85 90 95  
 10 Phe Leu Asp Ala Tyr Arg Arg Tyr Ser Gly Pro Trp Ser Lys Ile Tyr  
 100 105 110  
 Phe Val Leu Trp Trp Leu Val Ser Ser Val Ile Trp Val Asn Leu Phe  
 115 120 125  
 Leu Ala Leu Ile Leu Glu Asn Phe Leu His Lys Trp Asp Pro Arg Ser  
 130 135 140  
 20 His Leu Gln Pro Leu Ala Gly Thr Pro Glu Ala Thr Tyr Gln Met Thr  
 145 150 155 160  
 Val Glu Leu Leu Phe Arg Asp Ile Leu Glu Glu Pro Gly Glu Asp Glu  
 165 170 175  
 25 Leu Thr Glu Arg Leu Ser Gln His Pro His Leu Trp Leu Cys Arg Xaa  
 180 185 190

30

- 35 (2) INFORMATION FOR SEQ ID NO: 413:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Asn Val Val Val Val Ala Phe Gly Leu Ile Leu Ile Ile Glu Ser Leu  
 1 5 10 15  
 45 Gly Glu Gln Cys Pro  
 20

- 50 (2) INFORMATION FOR SEQ ID NO: 414:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 55 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys  
 1 5 10 15  
 60

Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala  
                     20                    25                    30  
 5 Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg  
                     35                    40                    45  
 Ala Pro Xaa  
                     50

10

(2) INFORMATION FOR SEQ ID NO: 415:

15 (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 32 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

20 Met Leu Ile Ile Ser Leu Arg Pro Gln Phe Pro Ser Leu Ile Val Gln  
       1                    5                    10                    15  
 Leu Glu Cys Ser Val Leu Phe Leu Pro Ile Ser Leu Asn Leu Leu Leu  
                     20                    25                    30  
 25

30

(2) INFORMATION FOR SEQ ID NO: 416:

35 (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 163 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu  
       1                    5                    10                    15  
 Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu  
                     20                    25                    30  
 45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp  
                     35                    40                    45  
 Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr  
                     50                    55                    60  
 50 Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu  
                     65                    70                    75                    80  
 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu  
                     85                    90                    95  
 55 Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg  
                     100                    105                    110  
 60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

115 120 125

Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg  
 130 135 140

5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Ile Gly Arg Pro  
 145 150 155 160

10 Gln Val Xaa

15 (2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe  
 1 5 10 15

25 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly  
 20 25 30

Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser  
 35 40 45

30 Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr  
 50 55 60

Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser  
 35 65 70 75 80

Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln  
 85 90 95

40 Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val  
 100 105 110

Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu  
 115 120 125

45 Ala Pro Gly Arg Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro  
 130 135 140

50 Trp Phe Thr Ala Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys  
 145 150 155 160

Arg Gln Arg Arg Gln Glu Arg Arg Gln Met Lys Arg Leu Xaa  
 165 170

55 (2) INFORMATION FOR SEQ ID NO: 418:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

605

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

5 Met Glu Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Val Ala Met Met  
 1 5 10 15  
 Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala Leu Arg  
 20 25 30  
 10 Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Cys Cys Leu  
 35 40 45  
 15 Ala Xaa  
 50

(2) INFORMATION FOR SEQ ID NO: 419:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Leu Gly Lys Gly Gly Gly Arg Ala Gly Leu Leu Arg Tyr Arg Leu  
 1 5 10 15  
 30 Leu Tyr Phe Thr Leu Val Val Gly Glu Gly Glu Pro Gly Glu Asn Lys  
 20 25 30  
 Val Thr Ile Pro Phe Phe Glu Thr Gly Lys Lys Ile Ile Phe Cys Ser  
 35 40 45  
 35 Val Lys Met Val Glu Asn Ser Asn Val Pro Ser His Lys Gly Pro Val  
 50 55 60  
 40 Pro Leu Arg Ser Glu Gln Trp Glu Leu Lys Ile Ser Glu Thr Leu Gly  
 65 70 75 80  
 Glu Gly Lys Ile Gly Phe Leu Leu Ile Gly Arg Cys Ser Ser Gly Xaa  
 85 90 95  
 45 Gly Gly Leu Cys Phe Cys Trp Asp Val Leu Cys Cys Met Tyr Ala Tyr  
 100 105 110  
 50 Met Asp Arg Ser Leu Leu Ser Leu  
 115 120

(2) INFORMATION FOR SEQ ID NO: 420:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:



606

Met Thr His Leu Leu Leu Thr Ala Thr Val Thr Pro Ser Glu Gln Asn  
 1 5 10 15  
 Ser Ser Arg Glu Pro Gly Trp Glu Thr Ala Met Ala Lys Asp Ile Leu  
 5 20 25 30  
 Gly Glu Ala Gly Leu His Phe Asp Glu Leu Asn Lys Leu Arg Val Leu  
 35 40 45  
 Asp Pro Glu Val Thr Gln Gln Thr Ile Glu Leu Lys Glu Glu Cys Lys  
 10 50 55 60  
 Asp Phe Val Asp Lys Ile Gly Gln Phe Gln Lys Ile Val Gly Gly Leu  
 65 70 75 80  
 Ile Glu Leu Val Asp Gln Leu Ala Lys Glu Ala Glu Asn Glu Lys Met  
 15 85 90 95  
 Lys Ala Ile Gly Ala Arg Asn Leu Leu Lys Ser Ile Ala Lys Gln Arg  
 20 100 105 110  
 Glu Ala Gln Gln Gln Gln Leu Gln Ala Leu Ile Ala Glu Lys Lys Met  
 115 120 125  
 Gln Leu Glu Arg Tyr Arg Val Glu Tyr Glu Ala Leu Cys Lys Val Glu  
 25 130 135 140  
 Ala Glu Gln Asn Glu Phe Ile Asp Gln Phe Ile Phe Gln Lys Xaa  
 145 150 155  
 30

## (2) INFORMATION FOR SEQ ID NO: 421:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 154 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val  
 1 5 10 15  
 Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu  
 45 20 25 30  
 Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala  
 35 40 45  
 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu  
 50 55 60  
 His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala  
 65 70 75 80  
 Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr  
 85 90 95  
 Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu  
 60 100 105 110

Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr  
 115 120 125

5 Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly  
 130 135 140

Val Arg Ile Phe Gly Ile Asn Lys Tyr Xaa  
 145 150

10

(2) INFORMATION FOR SEQ ID NO: 422:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 204 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

20 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala Leu  
 1 5 10 15

25 Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Ile Gly Ile Ala Ala  
 20 25 30

Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val Val Gly Val  
 35 40 45

30 Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala Leu Val Gly Leu  
 50 55 60

Ile Gly Ala Val Lys His His Gln Val Leu Leu Phe Phe Tyr Met Ile  
 65 70 75 80

35 Ile Leu Leu Leu Val Phe Ile Val Gln Phe Ser Val Ser Cys Ala Cys  
 85 90 95

40 Leu Ala Leu Asn Gln Glu Gln Gln Gly Gln Leu Leu Glu Val Gly Trp  
 100 105 110

Asn Asn Thr Ala Ser Ala Arg Asn Asp Ile Gln Arg Asn Leu Asn Cys  
 115 120 125

45 Cys Gly Phe Arg Ser Val Asn Pro Asn Asp Thr Cys Leu Ala Ser Cys  
 130 135 140

Val Lys Ser Asp His Ser Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu  
 145 150 155 160

50 Tyr Ala Gly Glu Val Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe  
 165 170 175

Ser Phe Thr Glu Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn  
 180 185 190

Gln Lys Asp Pro Arg Ala Asn Pro Ser Ala Phe Leu  
 195 200

60

## (2) INFORMATION FOR SEQ ID NO: 423:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

5 Met Leu Gln Ser Ile Ile Lys Asn Ile Trp Ile Pro Met Lys Pro Tyr  
 1 5 10 15  
 Tyr Thr Lys Val Tyr Gln Glu Ile Trp Ile Gly Met Gly Leu Met Gly  
 20 25 30  
 15 Phe Ile Val Tyr Lys Ile Arg Ala Ala Asp Lys Arg Ser Lys Ala Leu  
 35 40 45  
 Lys Ala Ser Ala Pro Ala Pro Gly His His Asn Gln Ile Tyr Leu Glu  
 20 50 55 60  
 Tyr Met Xaa  
 65

## (2) INFORMATION FOR SEQ ID NO: 424:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

35 Met Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val  
 1 5 10 15  
 Ala Val Asn Asn Pro Lys Lys Gln Glu  
 20 25  
 40

## (2) INFORMATION FOR SEQ ID NO: 425:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

45 Met Ala Ala Xaa Glu Pro Ala Val Leu Ala Leu Pro Asn Ser Gly Ala  
 1 5 10 15  
 Gly Gly Ala Gly Ala Pro Ser Gly Thr Val Pro Val Leu Phe Cys Phe  
 50 20 25 30  
 Ser Val Phe Ala Arg Pro Ser Ser Val Pro His Gly Ala Gly Tyr Glu  
 35 40 45  
 60 Leu Leu Ile Gln Lys Phe Leu Ser Leu Tyr Gly Asp Gln Ile Asp Met

609

50                      55                      60

His Arg Lys Phe Val Val Gln Leu Phe Ala Glu Glu Trp Gly Gln Tyr  
65                      70                      75                      80

5 Val Asp Leu Pro Lys Gly Phe Ala Val Ser Glu Arg Cys Lys Val Arg  
                    85                      90                      95

10 Leu Val Pro Leu Gln Ile Gln Leu Thr Thr Leu Gly Asn Leu Thr Pro  
                    100                      105                      110

Ser Ser Thr Val Phe Phe Cys Cys Asp Met Gln Glu Arg Phe Arg Pro  
115                      120                      125

15 Ala Ile Lys Tyr Phe Gly Asp Ile Ile Ser Val Gly Gln Arg Leu Leu  
130                      135                      140

Gln Gly Ala Arg Ile Leu Gly Ile Pro Val Ile Val Thr Glu Gln Tyr  
145                      150                      155                      160

20 Pro Lys Gly Leu Gly Ser Thr Val Gln Glu Ile Asp Leu Thr Gly Val  
                    165                      170                      175

25 Lys Leu Val Leu Pro Lys Thr Lys Phe Ser Met Val Leu Pro Glu Val  
180                      185                      190

Glu Ala Ala Leu Ala Glu Ile Pro Gly Val Arg Ser Val Val Leu Phe  
195                      200                      205

30 Gly Val Glu Thr His Val Cys Ile Gln Gln Thr Ala Leu Glu Leu Val  
210                      215                      220

Gly Arg Gly Val Glu Val His Ile Val Ala Asp Ala Thr Ser Ser Arg  
225                      230                      235                      240

35 Ser Met Met Asp Arg Met Phe Ala Leu Glu Arg Leu Ala Xaa Xaa Gly  
                    245                      250                      255

40 Ile Ile Val Thr Thr Ser Glu Ala Val Leu Leu Gln Leu Val Ala Asp  
260                      265                      270

Lys Asp His Pro Lys Phe Lys Glu Ile Gln Asn Leu Ile Lys Ala Ser  
275                      280                      285

45 Ala Pro Glu Ser Gly Leu Leu Ser Lys Val Xaa  
290                      295

50 (2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Arg Asp Leu Gly Thr Leu Leu Ser Pro Val Cys Ser  
1                      5                      10

60

## (2) INFORMATION FOR SEQ ID NO: 427:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

10

Met Phe Gly Cys Leu Val Ala Gly Arg Leu Val Gln Thr Ala Ala Gln  
 1 5 10 15

15

Gln Val Ala Glu Asp Lys Phe Val Phe Asp Leu Pro Asp Tyr Glu Ser  
 20 25 30

Ile Asn His Val Val Val Phe Met Leu Gly Thr Ile Pro Phe Pro Glu  
 35 40 45

20

Gly Met Gly Gly Ser Val Tyr Phe Ser Tyr Pro Asp Ser Asn Gly Met  
 50 55 60

Pro Val Trp Gln Leu Leu Gly Phe Val Thr Asn Gly Lys Pro Ser Ala  
 65 70 75 80

25

Ile Phe Lys Ile Ser Gly Leu Lys Ser Gly Glu Gly Ser Gln His Pro  
 85 90 95

30

Phe Gly Ala Met Asn Ile Val Arg Thr Pro Ser Val Ala Gln Ile Gly  
 100 105 110

Ile Ser Val Glu Leu Leu Asp Ser Met Ala Gln Gln Thr Pro Val Gly  
 115 120 125

35

Asn Ala Ala Val Ser Ser Val Asp Ser Phe Thr Gln Phe Thr Gln Lys  
 130 135 140

Met Leu Asp Asn Phe Tyr Asn Phe Ala Ser Ser Phe Ala Val Ser Gln  
 145 150 155 160

40

Ala Gln Met Thr Pro Ser Pro Ser Glu Met Phe Ile Pro Ala Asn Val  
 165 170 175

Val Leu Lys Trp Tyr Glu Asn Phe Gln Arg Arg Leu Ala Gln Asn Pro  
 180 185 190

45

Xaa Phe Trp Xaa Thr Xaa  
 195

50

## (2) INFORMATION FOR SEQ ID NO: 428:

55

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

60

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser

1                      5                      10                      15  
 Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Leu Trp Lys  
                             20                      25                      30  
 5    Asn Arg Gly Gly Val Gly Arg Ser Val Met Ser Ala Val Glu Xaa  
                             35                      40                      45  
 10  
 (2) INFORMATION FOR SEQ ID NO: 429:  
       (i) SEQUENCE CHARACTERISTICS:  
           (A) LENGTH: 370 amino acids  
           (B) TYPE: amino acid  
           (D) TOPOLOGY: linear  
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:  
 15  
 Met Lys Lys Val Glu Glu Lys Arg Val Asp Val Asn Ser Ala Val Ala  
 20    1                              5                              10                              15  
 Met Gly Glu Val Ile Leu Ala Val Cys His Pro Asp Cys Ile Thr Thr  
                             20                              25                              30  
 25    Ile Lys His Trp Ile Thr Ile Ile Arg Ala Arg Phe Glu Glu Val Leu  
                             35                              40                              45  
 Thr Trp Ala Lys Gln His Gln Gln Arg Leu Glu Thr Ala Leu Ser Glu  
                             50                              55                              60  
 30    Leu Val Ala Asn Ala Glu Leu Leu Glu Glu Leu Leu Ala Trp Ile Gln  
                             65                              70                              75                              80  
 Trp Ala Glu Thr Thr Leu Ile Gln Arg Asp Gln Glu Pro Ile Pro Gln  
 35                              85                              90                              95  
 Asn Ile Asp Arg Val Lys Ala Leu Ile Ala Glu His Gln Thr Phe Met  
                             100                              105                              110  
 40    Glu Glu Met Thr Arg Lys Gln Pro Asp Val Asp Arg Val Thr Lys Thr  
                             115                              120                              125  
 Tyr Lys Arg Lys Asn Ile Glu Pro Thr His Ala Pro Phe Ile Glu Lys  
                             130                              135                              140  
 45    Ser Arg Ser Gly Gly Arg Lys Ser Leu Ser Gln Pro Thr Pro Pro Pro  
                             145                              150                              155                              160  
 Met Pro Ile Leu Ser Gln Ser Glu Ala Lys Asn Pro Arg Ile Asn Gln  
 50                              165                              170                              175  
 Leu Ser Ala Arg Trp Gln Gln Val Trp Leu Leu Ala Leu Glu Arg Gln  
                             180                              185                              190  
 55    Arg Lys Leu Asn Asp Ala Leu Asp Arg Leu Glu Glu Leu Lys Glu Phe  
                             195                              200                              205  
 Ala Asn Phe Asp Phe Asp Val Trp Arg Lys Lys Tyr Met Arg Trp Met  
                             210                              215                              220  
 60

Asn His Lys Lys Ser Arg Val Met Asp Phe Phe Arg Arg Ile Asp Lys  
 225 230 235 240  
 5 Asp Gln Asp Gly Lys Ile Thr Arg Gln Glu Phe Ile Asp Gly Ile Leu  
 245 250 255  
 Ala Ser Lys Phe Pro Thr Thr Lys Leu Glu Met Thr Ala Val Ala Asp  
 260 265 270  
 10 Ile Phe Asp Arg Asp Gly Asp Gly Tyr Ile Asp Tyr Tyr Glu Phe Val  
 275 280 285  
 Ala Ala Leu His Pro Asn Lys Asp Ala Tyr Arg Pro Thr Thr Asp Ala  
 290 295 300  
 15 Asp Lys Ile Glu Asp Glu Val Thr Arg Gln Val Ala Gln Cys Lys Cys  
 305 310 315 320  
 Ala Lys Arg Phe Gln Val Glu Gln Ile Gly Glu Asn Lys Tyr Arg Phe  
 325 330 335  
 20 Phe Leu Gly Asn Gln Phe Gly Asp Ser Gln Gln Leu Arg Leu Val Arg  
 340 345 350  
 25 Ile Leu Arg Asn Arg Asp Gly Ser Arg Trp Trp Arg Met Asp Gly Leu  
 355 360 365  
 Gly Xaa  
 370  
 30

## (2) INFORMATION FOR SEQ ID NO: 430:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Asn Val Lys Thr Phe Ser Xaa Asp His Met His Phe Leu Cys Cys  
 1 5 10 15  
 45 Leu Tyr Leu Arg Tyr Val Thr Phe Val Tyr Leu Asn Leu Phe  
 20 25 30

## (2) INFORMATION FOR SEQ ID NO: 431:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Glu Pro His Leu Arg Cys Arg Val Thr Arg Val Arg Gly Ser Leu  
 1 5 10 15  
 60 Gly Asn Thr Gly Arg Trp Leu Leu

## 5 (2) INFORMATION FOR SEQ ID NO: 432:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met His Tyr Leu Val Leu Gly Gly Leu Gly Val Phe Leu Phe Phe Ser  
 1 5 10 15  
 Cys Phe Val Phe Leu Phe Phe Xaa Phe Ser Phe Ala Phe Phe Pro Phe  
 20 25 30  
 Tyr Leu Glu Gly Met Gly Gly Ser Gly Asn Arg Glu Val Gly Gly Gly  
 35 40 45  
 Phe Cys Leu Phe Phe  
 50

25

## (2) INFORMATION FOR SEQ ID NO: 433:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Val Ser Lys Ala Leu Leu Arg Leu Val Ser Ala Val Asn Arg Arg  
 1 5 10 15  
 Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser  
 20 25 30  
 Val Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu  
 35 40 45  
 Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu  
 45 50 55 60  
 Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val  
 65 70 75 80  
 Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Ile Thr Gly Gly  
 85 90 95  
 Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys Leu Met Met Asp Gly  
 100 105 110  
 His Glu Val Thr Val Val Asp Asn Phe Phe Thr Gly Arg Lys Arg Asn  
 115 120 125  
 Val Glu His Trp Ile Gly His Glu Asn Phe Glu Leu Ile Asn His Asp  
 130 135 140

60



Val Trp Ser Pro Ser Thr Ser Arg Leu Thr Arg Tyr Thr Ile Trp His  
145 150 155 160

5 Leu Gln Pro Pro Leu Gln Thr Thr Cys Ile Ile Leu Ser Arg His Xaa  
165 170 175

10

(2) INFORMATION FOR SEQ ID NO: 434:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

20

Met Leu Arg Cys Trp Pro Leu Phe Trp Leu Pro Leu Val Ser Pro Phe  
1 5 10 15

25

Cys Ser Leu Phe Trp Leu Leu Val Glu Trp Phe Gly Thr Asn Ile Asp  
20 25 30

Arg Glu Ser Tyr Asp Ala Ile Gly Gly Pro Ser Trp Met Thr Ala Ser  
35 40 45

30

Ser Phe Cys Leu Ser Asn Ser Asn Ile Trp Ser Leu Glu Ile Ser Ser  
50 55 60

Gly Ser Thr Ser Val Val His Ser Gln Gln Ala Met Asp  
65 70 75

35

(2) INFORMATION FOR SEQ ID NO: 435:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

45

Met Arg Ser Cys Glu Ile Gln Leu Cys Val Trp Leu Leu Val Ser Ser  
1 5 10 15

50

His Val Asp Met Val Leu Gly Gly Ser Pro Ser Thr Leu Tyr Met Met  
20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 436:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

5 Met Val Val Asn Ser Leu Cys Phe Leu Ser Leu Leu Val Ile Leu  
 1 5 10 15  
 Glu Leu Ser Thr Asp Ser Ser Ala Arg Leu Leu Tyr His Glu  
 20 25 30  
 10

(2) INFORMATION FOR SEQ ID NO: 437:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 69 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

20 Met Asp Lys Gln Lys His Leu Glu Val Arg Arg Ser Val Phe Lys Ile  
 1 5 10 15  
 Gln Gly Lys Ile Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser  
 25 20 25 30  
 Pro Thr Ile Phe Ser His Ser Ile Leu Leu Leu Leu Pro His His Val  
 35 40 45  
 30 Leu Pro Cys Thr Pro Gln Met Val Arg Gly Val Thr Gln Val Leu Arg  
 50 55 60  
 Glu Phe Gly Asp Gln  
 65  
 35

(2) INFORMATION FOR SEQ ID NO: 438:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 19 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

45 Met Pro Leu Cys Phe Phe Ser Phe Leu Cys Cys Trp Val Leu Val Phe  
 1 5 10 15  
 Lys Leu Ile  
 50

(2) INFORMATION FOR SEQ ID NO: 439:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 43 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg  
 1 5 10 15  
 5 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg  
 20 25 30  
 Arg Val Met Val Asn Leu Asn Ile Leu Phe Xaa  
 35 40  
 10

## (2) INFORMATION FOR SEQ ID NO: 440:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

20 Met Leu Leu Phe Pro Ser Leu Leu Phe Ala Ala Thr Tyr Asn Val Ala  
 1 5 10 15  
 25 Asn Pro Ser Arg Leu Ile Leu Tyr Met Ile Ser Ala Gly Ala Asp Ser  
 20 25 30  
 Gln

30

## (2) INFORMATION FOR SEQ ID NO: 441:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 53 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

40 Met Trp Gln Val Arg Gly Leu Pro Pro Val Pro Leu Leu Leu Thr Met  
 1 5 10 15  
 Ser Pro Pro Pro Cys Leu Ser Ser Pro Phe Pro Phe Ile Ser Val Pro  
 20 25 30  
 45 Leu Phe Glu Ala Val Pro Ile Ser Val Ser Asp Gln Pro Ser Pro Xaa  
 35 40 45  
 50 Leu Thr Thr Leu Leu  
 50

## (2) INFORMATION FOR SEQ ID NO: 442:

- 55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Ile Thr Ser Val Leu Val Phe Leu Ile Phe Phe Phe Pro Tyr Leu  
 1 5 10 15  
 5 Ser Leu Val Thr Leu Leu Gln Ala Arg Asn Leu Trp Val Ile His Arg  
 20 25 30  
 Ala Ala Leu Cys Glu Ser Gly Leu Phe His Trp Arg Lys Gly Ile Glu  
 35 40 45  
 10 Asn Gln Leu Glu Pro Met Tyr Phe Leu Pro His Gly Thr Leu Phe Leu  
 50 55 60

15

(2) INFORMATION FOR SEQ ID NO: 443:  
 20

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Leu Tyr Ser Cys Glu Pro Tyr Leu Ile Ile Leu Asn Ile Tyr Ser  
 1 5 10 15  
 30 Gln Lys Ala Phe Tyr Phe Tyr Phe Phe Glu Gly Ser Phe Ser Val Cys  
 20 25 30  
 Thr Leu

35

(2) INFORMATION FOR SEQ ID NO: 444:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 89 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Arg Gln Arg Gln Ala Ala Cys Gln Pro Pro Pro Ser Arg Asn Gly  
 1 5 10 15  
 50 Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val  
 20 25 30  
 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Ser Ser Pro Leu  
 35 40 45  
 55 Asn Leu Leu Leu Leu Val Ser Ile Ser Trp Asp Leu Gly Leu Lys Leu  
 50 55 60  
 Asn Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr  
 65 70 75 80

60

Lys Lys Phe Asn Lys Lys Lys Lys  
85

5

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

15 Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
20 25 30

20 Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
25 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
65 70 75 80

30 Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala  
100 105 110

35 Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
40 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
145 150 155 160

45 Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
180 185 190

50 Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr  
55 210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
225 230 235 240

60 Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
260 265 270

5 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Pro Pro Gly Pro Glu Lys Ser  
290 295 300

10

Gly Asn Pro Arg Thr Pro Ser Thr Leu Thr Ser Gln Gly Gln Gly Arg  
305 310 315 320

15

Glu Ala Ala Leu Leu Gly Leu Leu Thr Leu Gln Gly Thr Val Ala Phe  
325 330 335

Val Glu Thr Leu Met Glu Ile Cys Leu Thr Ser Gly Lys Asp  
340 345 350

20

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

30 Met Val Phe Leu Pro Arg Gly Val Val Val Ser Gly Gly Ala Ala Cys  
1 5 10 15

Leu Trp Leu Thr Phe Ile Leu Glu Thr Glu Val Tyr Leu Asp Leu Ala  
20 25 30

35

Thr Glu Ala Arg Ala His Ser Arg Met Gly Leu Gly Leu Trp Pro Pro  
35 40 45

Asn

40

(2) INFORMATION FOR SEQ ID NO: 447:

45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 278 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Ser Ala Glu Leu Asp Tyr Thr Ile Glu Ile Pro Asp Gln Pro  
1 5 10 15

55

Cys Trp Ser Gln Lys Asn Ser Pro Ser Pro Gly Gly Lys Glu Ala Glu  
20 25 30

Thr Arg Gln Pro Val Val Ile Leu Leu Gly Trp Gly Gly Cys Lys Asp  
35 40 45

60

620

Lys Asn Leu Ala Lys Tyr Ser Ala Ile Tyr His Lys Arg Gly Cys Ile  
 50 55 60  
 Val Ile Arg Tyr Thr Ala Pro Trp His Met Val Phe Phe Ser Glu Ser  
 5 65 70 75 80  
 Leu Gly Ile Pro Ser Leu Arg Val Leu Ala Gln Lys Leu Leu Glu Leu  
 85 90 95  
 10 Leu Phe Asp Tyr Glu Ile Glu Lys Glu Pro Leu Leu Phe His Val Phe  
 100 105 110  
 Ser Asn Gly Gly Val Met Leu Tyr Arg Tyr Val Leu Glu Leu Leu Gln  
 115 120 125  
 15 Thr Arg Arg Phe Cys Arg Leu Arg Val Val Gly Thr Ile Phe Asp Ser  
 130 135 140  
 Ala Pro Gly Asp Ser Asn Leu Val Gly Ala Leu Arg Ala Leu Ala Ala  
 20 145 150 155 160  
 Ile Leu Glu Arg Arg Ala Ala Met Leu Arg Leu Leu Leu Val Ala  
 165 170 175  
 25 Phe Ala Leu Val Val Val Leu Phe His Val Leu Leu Ala Pro Ile Thr  
 180 185 190  
 Ala Xaa Phe His Thr His Phe Tyr Asp Arg Leu Gln Asp Ala Gly Ser  
 195 200 205  
 30 Arg Trp Pro Glu Leu Tyr Leu Tyr Ser Arg Ala Asp Glu Val Val Leu  
 210 215 220  
 Ala Arg Asp Ile Glu Arg Met Val Glu Ala Arg Leu Ala Arg Arg Val  
 35 225 230 235 240  
 Leu Ala Arg Ser Val Asp Phe Val Ser Ser Ala His Val Ser His Leu  
 245 250 255  
 40 Arg Asp Tyr Pro Thr Tyr Tyr Thr Ser Leu Cys Val Asp Phe Met Arg  
 260 265 270  
 Asn Cys Val Arg Cys Xaa  
 275  
 45

(2) INFORMATION FOR SEQ ID NO: 448:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 199 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Ser Phe Ile Phe Asp Trp Ile Tyr Ser Gly Phe Ser Ser Val Leu  
 1 5 10 15  
 Gln Phe Leu Gly Leu Tyr Lys Lys Thr Gly Lys Leu Val Phe Leu Gly  
 60 20 25 30

Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp  
 35 40 45  
 5 Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu  
 50 55 60  
 Thr Ile Ala Gly Met Thr Phe Thr Thr Phe Asp Leu Gly Gly His Val  
 65 70 75 80  
 10 Gln Ala Arg Arg Val Trp Lys Asn Tyr Leu Pro Ala Ile Asn Gly Ile  
 85 90 95  
 15 Val Phe Leu Val Asp Cys Ala Asp His Glu Arg Leu Leu Glu Ser Lys  
 100 105 110  
 Glu Glu Leu Asp Ser Leu Met Thr Asp Glu Thr Ile Ala Asn Val Pro  
 115 120 125  
 20 Ile Leu Ile Leu Gly Asn Lys Ile Asp Arg Pro Glu Ala Ile Ser Glu  
 130 135 140  
 Glu Arg Leu Arg Glu Met Phe Gly Leu Tyr Gly Gln Thr Thr Gly Lys  
 145 150 155 160  
 25 Gly Ser Ile Ser Leu Lys Glu Leu Asn Ala Arg Pro Leu Glu Val Phe  
 165 170 175  
 30 Met Cys Ser Val Leu Lys Arg Gln Gly Tyr Gly Glu Gly Phe Arg Trp  
 180 185 190  
 Met Ala Gln Tyr Ile Asp Xaa  
 195

35

(2) INFORMATION FOR SEQ ID NO: 449:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

45

Met Thr Leu Ser Arg Phe Ala Tyr Asn Gly Lys Arg Cys Pro Ser Ser  
 1 5 10 15

50

Tyr Asn Ile Leu Asp Asn Ser Lys Ile Ile Ser Glu Glu Cys Arg Lys  
 20 25 30

Glu Leu Thr Ala Leu Leu His His Tyr Tyr Pro Ile Glu Ile Asp Pro  
 35 40 45

55

His Arg Thr Val Lys Glu Lys Leu Pro His Met Val Glu Trp Trp Thr  
 50 55 60

Lys Ala His Asn Leu Leu Cys Gln Gln Lys Ile Gln Lys Phe Gln Ile  
 65 70 75 80

60

Ala Gln Val Val Arg Glu Ser Asn Ala Met Leu Arg Glu Gly Tyr Lys



622

85                      90                      95  
 Thr Phe Phe Asn Thr Leu Tyr His Asn Asn Ile Pro Leu Phe Ile Phe  
                          100                      105                      110  
 5 Ser Ala Gly Ile Gly Asp Ile Leu Glu Glu Ile Ile Arg Gln Met Lys  
                          115                      120                      125  
 10 Val Phe His Pro Asn Ile His Ile Val Ser Asn Tyr Met Asp Phe Asn  
                          130                      135                      140  
 Glu Asp Gly Phe Leu Gln Gly Phe Lys Gly Gln Leu Ile His Thr Tyr  
                          145                      150                      155                      160  
 15 Asn Lys Asn Ser Ser Val Cys Glu Asn Xaa Gly Tyr Phe Gln Gln Leu  
    165                      170                      175  
 Glu Gly Lys Thr Asn Val Ile Leu Leu Gly Asp Ser Ile Gly Asp Leu  
    180                      185                      190  
 20 Thr Met Ala Asp Gly Val Pro Gly Val Gln Asn Ile Leu Lys Ile Gly  
    195                      200                      205  
 25 Phe Leu Asn Asp Lys Val Glu Glu Arg Arg Xaa Arg Tyr Met Asp Ser  
    210                      215                      220  
 Tyr Asp Ile Val Leu Glu Lys Asp Glu Thr Leu Asp Val Val Asn Gly  
    225                      230                      235                      240  
 30 Leu Leu Gln His Ile Leu Cys Gln Gly Val Gln Leu Glu Met Gln Gly  
    245                      250                      255  
 Pro Xaa

35

(2) INFORMATION FOR SEQ ID NO: 450:

40

- (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 87 amino acids  
     (B) TYPE: amino acid  
     (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Ser His Val Leu Leu Cys Pro Ser Leu Ser Cys Ser Asn Leu Leu  
     1                      5                      10                      15  
 50 Pro Pro Ser His Ser Leu Gly Thr Met Gly Ser Leu Ser Pro His Leu  
                          20                      25                      30  
 Cys Gly His Thr Met Cys Pro Val Asn Pro Glu Leu Pro Leu Ser Ser  
                          35                      40                      45  
 55 Arg Leu Thr Thr Asp Gln Pro Gln Pro Asp Ala Cys Ser Pro Thr Leu  
                          50                      55                      60  
 Leu Thr Leu Pro Leu Pro Ser Ser Phe Leu Pro His Ser Lys Pro Thr  
     65                      70                      75                      80  
 60

Phe Xaa His Pro Cys Ser Pro  
85

5

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

10

15

Met Phe Ser Ile Asn Pro Leu Glu Asn Leu Lys Val Tyr Ile Ser Ser  
1 5 10 15

Arg Pro Pro Leu Val Val Phe Met Ile Ser Val Xaa Pro Met Ala Ile  
20 25 30

20

Ala Phe Leu Thr Leu Gly Tyr Phe Phe Lys Ile Lys Glu Ile Lys Ser  
35 40 45

25

Pro Glu Met Ala Glu Asp Trp Asn Thr Phe Leu Leu Arg Phe Asn Asp  
50 55 60

Leu Asp Leu Cys Val Ser Glu Asn Glu Thr Leu Lys His Leu Thr Asn  
65 70 75 80

30

Asp Thr Thr Thr Pro Glu Ser Thr Met Thr Ser Gly Gln Ala Arg Ala  
85 90 95

Ser Thr Gln Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile  
100 105 110

35

Ser Val Ser Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly  
115 120 125

Tyr Ser Arg Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln  
130 135 140

40

Ile Gly Leu Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe  
145 150 155 160

45

Thr Leu Pro Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His  
165 170 175

Cys Glu Gln Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro  
180 185 190

50

Gly Val Phe Pro Val Thr Val Gln Pro Pro His Cys Val Pro Asp Thr  
195 200 205

Tyr Ser Asn Ala Thr Leu Trp Tyr Lys Ile Phe Thr Thr Ala Arg Asp  
210 215 220

55

Ala Asn Thr Lys Tyr Ala Gln Asp Tyr Asn Pro Phe Trp Cys Tyr Lys  
225 230 235 240

60

Gly Ala Ile Gly Lys Val Tyr His Ala Leu Asn Pro Lys Leu Thr Val  
245 250 255

Ile Val Pro Asp Asp Asp Arg Ser Leu Ile Asn Leu His Leu Met His  
260 265 270

5 Thr Ser Tyr Phe Leu Phe Val Met Val Ile Thr Met Phe Cys Tyr Ala  
275 280 285

Val Ile Lys Gly Arg Pro Ser Lys Leu Arg Gln Ser Asn Pro Glu Phe  
290 295 300

10

Cys Pro Glu Lys Val Ala Leu Ala Glu Ala Xaa  
305 310 315

15

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

25 Met Pro Gly Leu Ser Leu Ala Leu Leu Pro Phe Gly Pro Gly Cys Thr  
1 5 10 15

Glu Ala Leu His Ala Gly Cys Phe Pro Ala Phe Ala Ser Ala Thr Arg  
20 25 30

30 Val Asn Gly Glu Ala Ala Leu Ser Pro Gly Leu Cys Asp Pro Ile Ser  
35 40 45

Val Pro Tyr Val  
50

35

(2) INFORMATION FOR SEQ ID NO: 453:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

45

Met Ala Val Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys  
1 5 10 15

50 Gly Phe Ile Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val  
20 25 30

Leu Leu Trp Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala  
35 40 45

55 Gly Leu Lys Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys  
50 55 60

Asp Thr Glu Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys  
65 70 75 80

60

Asp Ser Asn Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala  
                             85                            90                            95  
 5 Ser Gln Met Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser  
                             100                            105                            110  
 Tyr Tyr Asn Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu  
                             115                            120                            125  
 10 Tyr Met Thr Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr  
                             130                            135                            140  
 Thr Gln Gly Leu Ser Gly Phe His Pro Gln Tyr Phe Asp Gly Ser Ile  
                             145                            150                            155                            160  
 15 Ser Tyr Asn Trp Asn Asn Gly Asn Cys Ser Phe Tyr Leu Ala Thr Ser  
                             165                            170                            175  
 Lys Met Trp Phe Gly Ser Ala Gly Leu Ile Ser Gly Leu Ala Gln Leu  
                             180                            185                            190  
 Ser Cys Leu Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro  
                             195                            200                            205  
 25 Leu Asp Leu Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile  
                             210                            215                            220  
 Gln Gly Glu Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu  
                             225                            230                            235                            240  
 30 Ile Tyr Met Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr  
                             245                            250                            255  
 Ser Pro Glu Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly  
                             260                            265                            270  
 Val Ile Ala Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr  
                             275                            280                            285  
 40 Gln Leu Leu Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn  
                             290                            295                            300  
 Gly Val Gln Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile  
                             305                            310                            315                            320  
 45 Met Val Ile Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu  
                             325                            330                            335  
 Ile Ser Val Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe  
                             340                            345                            350  
 Ala Gln Asn Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala  
                             355                            360                            365  
 55 Lys Glu Val Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val Xaa  
                             370                            375                            380

60 (2) INFORMATION FOR SEQ ID NO: 454:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

5 Met Arg Ser Ile Gly Asn Lys Asn Thr Ile Leu Leu Gly Leu Gly Phe  
 1 5 10 15  
 10 Gln Ile Leu Gln Leu Ala Trp Tyr Gly Phe Gly Ser Glu Pro Trp Met  
 20 25 30  
 15 Met Trp Ala Ala Gly Ala Val Ala Ala Met Ser Ser Ile Thr Phe Pro  
 35 40 45  
 20 Ala Val Ser Ala Leu Val Ser Arg Thr Ala Asp Ala Asp Gln Gln Gly  
 50 55 60  
 25 Val Val Gln Gly Met Ile Thr Gly Ile Arg Gly Leu Cys Asn Gly Leu  
 65 70 75 80  
 Gly Pro Ala Leu Tyr Gly Phe Ile Phe Tyr Ile Phe His Val Glu Leu  
 85 90 95  
 30 Lys Glu Leu Pro Ile Thr Gly Thr Asp Leu Gly Thr Asn Thr Ser Pro  
 100 105 110  
 Gln His His Phe Glu Gln Asn Ser Ile Ile Pro Gly Pro Pro Phe Leu  
 115 120 125  
 Phe Gly Ala Cys Ser Val Leu Leu Ala Leu Leu Val Ala Leu Phe Ile  
 130 135 140  
 35 Pro Glu His Thr Asn Leu Ser Leu Arg Ser Ser Ser Trp Arg Lys His  
 145 150 155 160  
 Cys Gly Ser His Ser His Pro His Asn Thr Gln Ala Pro Gly Glu Ala  
 165 170 175  
 40 Lys Glu Pro Leu Leu Gln Asp Thr Asn Val  
 180 185

## (2) INFORMATION FOR SEQ ID NO: 455:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

55 Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu  
 1 5 10 15  
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln  
 20 25 30  
 60 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala

35                      40                      45  
 Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe  
 50                      55                      60  
 5 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly  
 65                      70                      75                      80  
 10 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His  
 85                      90                      95  
 Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp  
 100                      105                      110  
 15 Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val  
 115                      120                      125  
 Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro  
 130                      135                      140  
 20 His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val  
 145                      150                      155                      160  
 25 Arg Arg Xaa

30 (2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Arg Ile Gln Val Phe Ile Leu Leu Leu Gly Ala Gly Gly Thr Ser  
 1                      5                      10                      15  
 40 Gln Phe Thr Lys Pro Pro Ser Leu Pro Leu Glu Pro Glu Pro Ala Val  
 20                      25                      30  
 Glu Ser Ser Pro Thr Glu Thr Ser Glu Gln Ile Arg Glu Lys  
 35                      40                      45  
 45

(2) INFORMATION FOR SEQ ID NO: 457:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Ser Tyr Leu Ala Phe Leu Tyr Met Thr Phe Asp Phe Cys Cys Leu  
 1                      5                      10                      15  
 60 Tyr Phe Ser Thr Val Tyr Ala Pro Ser Phe Lys Tyr Ile Cys Val His  
 20                      25                      30

Thr Asp Thr His Ile Cys Val Cys Val Cys Ile Tyr Leu Ser Ser Val  
 35 40 45

5 Val Ser Lys Ser Ser Ala Glu Ala Asp Gly Val Leu Gln Pro Arg Arg  
 50 55 60

His Pro Ala Ser Leu Leu Ile Val Phe Ala Thr Ser Ile Ser Glu Ser  
 65 70 75 80

10 Ser Leu Leu Ile Phe Ser Phe Gln Lys Thr Glu Ala Lys Leu Ile Val  
 85 90 95

15 Phe Ala Val Ser Leu Ala Ala Lys Xaa  
 100 105

20 (2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser  
 1 5 10 15

30 Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val  
 20 25 30

Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro  
 35 40 45

35 Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln  
 50 55 60

40 Ala His Thr Val Ala Xaa  
 65 70

45 (2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe  
 1 5 10 15

55 Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val  
 20 25 30

Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro  
 35 40 45

60

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala  
 50 55 60

5 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro  
 65 70 75 80

Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met  
 85 90 95

10 Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys  
 100 105 110

Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly  
 115 120 125

15 Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys  
 130 135 140

20 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa  
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 460:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 332 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser  
 1 5 10 15

35 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly  
 20 25 30

Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu  
 35 40 45

40 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp  
 50 55 60

45 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu  
 65 70 75 80

Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu  
 85 90 95

50 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser  
 100 105 110

Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr  
 115 120 125

55 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile  
 130 135 140

60 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser  
 145 150 155 160



630

Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His  
 165 170 175

5 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu  
 180 185 190

Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn  
 195 200 205

10 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser  
 210 215 220

Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu  
 15 225 230 235 240

Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser  
 245 250 255

20 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu  
 260 265 270

Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg  
 275 280 285

25 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met  
 290 295 300

Thr Phe Phe Pro Lys Glu Arg Val Phe Ser Asp Lys Gly Cys Lys  
 30 305 310 315 320

Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp  
 325 330

35

(2) INFORMATION FOR SEQ ID NO: 461:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

45 Met Leu Lys Cys Ile  
 1 5

50 (2) INFORMATION FOR SEQ ID NO: 462:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ile Leu Thr Leu Leu Ser Val Val Ser Thr Met Ala Ser  
 1 5 10  
 60

(2) INFORMATION FOR SEQ ID NO: 463:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Lys Leu His Pro Pro Pro Pro Ser Pro Val Thr Gln Asp His Arg  
 1 5 10 15  
 Ser Lys Ser Ser His Ser Asn Trp Met Pro Arg Met Gly Ala Cys Ser  
 20 25 30  
 Met Ser Arg Thr Ser Ser Ser Gly Pro Pro Ser Leu Cys Lys Ser Thr  
 35 40 45  
 Ser Gly Arg Ser Cys Thr Arg Pro His Cys Trp Pro Ser Leu Pro Ala  
 50 55 60  
 Trp Val Ser Val Phe Thr Arg Thr Asn Thr Gly Ser Trp Cys Tyr Pro  
 65 70 75 80  
 Ala Trp Gly Gly Ala Phe Ser Arg Pro Trp Met Ser Ala Gln Ser Met  
 85 90 95  
 Cys Cys Ala Glu Arg Ser Val Leu Gln Val Ala Cys Arg Leu Leu Asp  
 100 105 110  
 Ala Leu Glu Phe Leu His Glu Asn Glu Tyr Val His Gly Asn Val Thr  
 115 120 125  
 Ala Glu Asn Ile Phe Val Asp Pro Glu Asp Gln Ser Gln Val Thr Leu  
 130 135 140  
 Ala Gly Tyr Gly Phe Ala Phe Arg Tyr Cys Pro Ser Gly Lys His Val  
 145 150 155 160  
 Ala Tyr Val Glu Gly Ser Arg Ser Pro His Glu Gly Asp Leu Glu Phe  
 165 170 175  
 Ile Ser Met Asp Leu His Lys Gly Cys Gly Pro Ser Arg Arg Xaa Asp  
 180 185 190  
 Leu Gln Ser Leu Gly Tyr Cys Met Leu Lys Trp Leu Tyr Gly Phe Leu  
 195 200 205  
 Pro Trp Thr Asn Cys Leu Pro Xaa Xaa Glu Asp Ile Met Lys Gln Lys  
 210 215 220  
 Gln Lys Phe Val Asp Lys Pro Gly Pro Phe Val Gly Pro Cys Gly His  
 225 230 235 240  
 Trp Ile Arg Pro Ser Glu Thr Leu Gln Lys Tyr Leu Lys Val Val Met  
 245 250 255  
 Ala Leu Thr Tyr Glu Glu Lys Pro Pro Tyr Ala Met Leu Arg Asn Asn  
 260 265 270

Leu Glu Ala Leu Leu Gln Asp Leu Arg Val Ser Pro Tyr  
 275 280 285

5

(2) INFORMATION FOR SEQ ID NO: 464:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

15

Met Thr Ser Pro Pro Pro His Gln Gly Trp Glu Gln Arg Gly Cys Gly  
 1 5 10 15

Glu Ser Gln Val Pro Leu Ala Leu Ser Arg Val Phe Ser Thr Ser His  
 20 25 30

20

Tyr Cys Leu Leu Leu Val Ala Asn Gln Ser Ile Phe Phe Pro Cys Leu  
 35 40 45

25

Trp Ala Val Glu Arg Leu Leu Gly Val Arg Cys Thr Cys Pro Leu Ser  
 50 55 60

Trp Gly Lys Arg Ile Ile Ser Glu His Cys Ser Ala Gln Ser Ser Xaa  
 65 70 75 80

30

35

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

Met His Thr Trp Tyr Asn Asp Arg Arg Gln Asn Cys His Cys Leu Leu  
 1 5 10 15

45

Phe Phe Leu Ile Tyr Leu Arg Lys Ile Tyr Gln Val Val Pro His Val  
 20 25 30

50

Pro Leu Leu Val Lys Cys Arg Gly Arg Leu Lys Gly Val Asn Ile  
 35 40 45

55

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val  
 1 5 10 15  
 5 Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr  
 20 25 30  
 Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu  
 35 40 45  
 10 Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser  
 50 55 60  
 Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu Glu Ala Gln Val Glu  
 15 65 70 75 80  
 Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro Gln Lys Ala Glu Asn Xaa  
 85 90 95  
 20  
 25 (2) INFORMATION FOR SEQ ID NO: 467:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 399 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:  
 Met Ala Ser Gly Ala Asp Ser Lys Gly Asp Asp Leu Ser Thr Ala Ile  
 1 5 10 15  
 35 Leu Lys Gln Lys Asn Arg Pro Asn Arg Leu Ile Val Asp Glu Ala Ile  
 20 25 30  
 Asn Glu Asp Asn Ser Val Val Ser Leu Ser Gln Pro Lys Met Asp Glu  
 40 35 40 45  
 Leu Gln Leu Phe Arg Gly Asp Thr Val Leu Leu Lys Gly Lys Lys Arg  
 50 55 60  
 45 Arg Glu Ala Val Cys Ile Val Leu Ser Asp Asp Thr Cys Ser Asp Glu  
 65 70 75 80  
 Lys Ile Arg Met Asn Arg Val Val Arg Asn Asn Leu Arg Val Arg Leu  
 85 90 95  
 50 Gly Asp Val Ile Ser Ile Gln Pro Cys Pro Asp Val Lys Tyr Gly Lys  
 100 105 110  
 Arg Ile His Val Leu Pro Ile Asp Asp Thr Val Glu Gly Ile Thr Gly  
 115 120 125  
 Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr Phe Leu Glu Ala Tyr Arg  
 130 135 140  
 60 Pro Ile Arg Lys Gly Asp Ile Phe Leu Val Arg Gly Gly Met Arg Ala

634

145	150	155	160
Val Glu Phe Lys Val Val Glu Thr Asp Pro Ser Pro Tyr Cys Ile Val	165	170	175
Ala Pro Asp Thr Val Ile His Cys Glu Gly Glu Pro Ile Lys Arg Glu	180	185	190
Asp Glu Glu Glu Ser Leu Asn Glu Val Gly Tyr Asp Asp Ile Gly Gly	195	200	205
Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu Met Val Glu Leu Pro Leu	210	215	220
Arg His Pro Ala Leu Phe Lys Ala Ile Gly Val Lys Pro Pro Arg Gly	225	230	235
Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Ile Ala Arg	245	250	255
Ala Val Ala Asn Glu Thr Gly Ala Phe Phe Phe Leu Ile Asn Gly Pro	260	265	270
Glu Ile Met Ser Lys Leu Ala Gly Glu Ser Glu Ser Asn Leu Arg Lys	275	280	285
Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro Ala Ile Ile Phe Ile Asp	290	295	300
Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu Lys Thr His Gly Glu Val	305	310	315
Glu Arg Arg Ile Val Ser Gln Leu Leu Thr Leu Met Asp Gly Leu Lys	325	330	335
Gln Arg Ala His Val Ile Val Met Ala Ala Thr Asn Arg Pro Asn Ser	340	345	350
Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg Phe Asp Arg Glu Val Asp	355	360	365
Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu Glu Ile Leu Gln Ile His	370	375	380
Thr Lys Asn Met Lys Leu Ala Asp Asp Val Asp Leu Glu Gln Xaa	385	390	395

50 (2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Leu

1

60

## (2) INFORMATION FOR SEQ ID NO: 469:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu  
 1 5 10 15  
 Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr  
 15 20 25 30  
 Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys  
 35 40 45  
 His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu  
 50 55 60  
 Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys  
 65 70 75 80  
 Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys  
 85 90 95  
 Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala  
 100 105 110  
 Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln  
 115 120 125  
 Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu  
 130 135 140  
 Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser  
 145 150 155 160  
 Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys  
 165 170 175  
 Ile Val Ile Phe Xaa Ser Lys Pro Arg Asn Pro Arg Tyr Ala Pro His  
 180 185 190  
 Leu Glu Pro Gly Ala Leu Pro Asn Leu Xaa Xaa Xaa Ser Leu Ser Lys  
 195 200 205  
 Met Ser Xaa Xaa Ser Xaa Met Arg Asn Ser Gln Ala His Arg Asn Phe  
 210 215 220  
 Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn  
 225 230 235 240  
 Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu  
 245 250 255  
 Leu Trp Ile Cys Cys Ala Thr Cys Cys Tyr Thr Leu Leu Asp Ala Val  
 260 265 270

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 470:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

15

Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe Ser  
 1 5 10 15

Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr Pro  
 20 25 30

20

Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala  
 35 40 45

25

Thr Glu Lys Arg Leu Thr Lys Leu Leu Val His Ser Ser Leu Val Gly  
 50 55 60

Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu Ser  
 65 70 75 80

30

Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu Leu Asp  
 85 90 95

Lys Asn Asn Ile Pro Thr Arg Ser Tyr Val Ser Tyr Phe Tyr His Asp  
 100 105 110

35

Ser Leu Tyr Thr Thr Asp Cys Tyr Thr Ala Lys Ala Ser Leu Ala Gly  
 115 120 125

40

Xaa Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Leu Ala  
 130 135 140

Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe Pro  
 145 150 155 160

45

Gly Ser Val Leu Phe Leu Pro His Ser Tyr Ile Gly Asn Ser Gly Met  
 165 170 175

Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr Ser  
 180 185 190

50

55

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

60

637

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

5 Met Arg Lys Thr Arg Leu Trp Gly Leu Leu Trp Met Leu Phe Val Ser  
 1 5 10 15  
 Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu Leu Lys  
 20 25 30  
 10 Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu Glu Lys Phe  
 35 40 45  
 Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro  
 50 55 60  
 15 Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val  
 65 70 75 80  
 Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu  
 85 90 95  
 Arg Val Arg Met Val Asn Leu Gln Val Glu Asp Ser Gly Leu Tyr Gln  
 100 105 110  
 25 Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg  
 115 120 125  
 Ile Arg Leu Val Val Thr Lys Gly Phe Ser Gly Thr Pro Gly Ser Asn  
 130 135 140  
 30 Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys  
 145 150 155 160  
 Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro  
 165 170 175  
 Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu  
 180 185 190  
 40 Thr Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile  
 195 200 205  
 Leu Leu Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu  
 210 215 220  
 45 Phe Ala Val Thr Leu Arg Ser Phe Val Pro  
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

60 Met Leu His Ile Leu Pro Leu Lys Ser Tyr Asp Phe Pro His Phe Ser  
 1 5 10 15



Leu Met Gly Arg Tyr Arg Cys Ala Ser Leu Leu Phe Cys Phe Leu Leu  
                   20                  25                  30  
 5 Leu Phe Phe Phe Phe Cys Ser Val Leu Trp Thr Phe Ser Asp Met His  
                   35                  40                  45  
 Arg Ser Gly Glu Asp Gly Pro Trp Thr Pro Cys Val His His Leu Ala  
                   50                  55                  60  
 10 Ala Ser Leu Ile Ser Tyr Gly Gln Pro Gly Phe Ile Cys Ile Ser Leu  
                   65                  70                  75                  80  
 Phe Ser Pro Val Leu Phe Ile Glu Asn Pro Arg His Tyr Ala Asn Ala  
                   85                  90                  95  
 15 Thr Val Thr Thr Leu Gly Asp Trp Xaa  
                   100                  105  
 20

(2) INFORMATION FOR SEQ ID NO: 473:

25 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 32 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

30 Met Val Phe Leu Lys Tyr Arg Phe Leu Phe Phe Leu Val Phe Leu Ala  
       1                  5                  10                  15  
 Asn Cys Ile Tyr Ser Leu His Tyr Lys Pro Ser Leu Met Tyr Pro Lys  
                   20                  25                  30  
 35

40 (2) INFORMATION FOR SEQ ID NO: 474:

45 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 571 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

50 Met Ala Leu Ser Arg Gly Leu Pro Arg Glu Leu Ala Glu Ala Val Ala  
       1                  5                  10                  15  
 Gly Gly Arg Val Leu Val Val Gly Ala Gly Gly Ile Gly Cys Glu Leu  
                   20                  25                  30  
 55 Leu Lys Asn Leu Val Leu Thr Gly Phe Ser His Ile Asp Leu Ile Asp  
                   35                  40                  45  
 Leu Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Gln  
                   50                  55                  60  
 60

Lys Lys His Val Gly Arg Ser Lys Ala Gln Val Ala Lys Glu Ser Val  
 65 70 75 80  
 5 Leu Gln Phe Tyr Pro Lys Ala Asn Ile Val Ala Tyr His Asp Ser Ile  
 85 90 95  
 Met Asn Pro Asp Tyr Asn Val Glu Phe Phe Arg Gln Phe Ile Leu Val  
 100 105 110  
 10 Met Asn Ala Leu Asp Asn Arg Ala Ala Arg Asn His Val Asn Arg Met  
 115 120 125  
 Cys Leu Ala Ala Asp Val Pro Leu Ile Glu Ser Gly Thr Ala Gly Tyr  
 130 135 140  
 15 Leu Gly Gln Val Thr Thr Ile Lys Lys Gly Val Thr Glu Cys Tyr Glu  
 145 150 155 160  
 Cys His Pro Lys Pro Thr Gln Arg Thr Phe Pro Gly Cys Thr Ile Arg  
 165 170 175  
 20 Asn Thr Pro Ser Glu Pro Ile His Cys Ile Val Trp Ala Lys Tyr Leu  
 180 185 190  
 25 Phe Asn Gln Leu Phe Gly Glu Glu Asp Ala Asp Gln Glu Val Ser Pro  
 195 200 205  
 Asp Arg Ala Asp Pro Glu Ala Ala Trp Glu Pro Thr Glu Ala Glu Ala  
 210 215 220  
 30 Arg Ala Arg Ala Ser Asn Glu Asp Gly Asp Ile Lys Arg Ile Ser Thr  
 225 230 235 240  
 Lys Glu Trp Ala Lys Ser Thr Gly Tyr Asp Pro Val Lys Leu Phe Thr  
 245 250 255  
 35 Lys Leu Phe Lys Asp Asp Ile Arg Tyr Leu Leu Thr Met Asp Lys Leu  
 260 265 270  
 40 Trp Arg Lys Arg Lys Pro Pro Val Pro Leu Asp Trp Ala Glu Val Gln  
 275 280 285  
 Ser Gln Gly Glu Glu Thr Asn Ala Ser Asp Gln Gln Asn Glu Pro Gln  
 290 295 300  
 45 Leu Gly Leu Lys Asp Gln Gln Val Leu Asp Val Lys Ser Tyr Ala Arg  
 305 310 315 320  
 Leu Phe Ser Lys Ser Ile Glu Thr Leu Arg Val His Leu Ala Glu Lys  
 325 330 335  
 50 Gly Asp Gly Ala Glu Leu Ile Trp Asp Lys Asp Asp Pro Ser Ala Met  
 340 345 350  
 55 Asp Phe Val Thr Ser Ala Ala Asn Leu Arg Met His Ile Phe Ser Met  
 355 360 365  
 60 Asn Met Lys Ser Arg Phe Asp Ile Lys Ser Met Ala Gly Asn Ile Ile  
 370 375 380

640

Pro Ala Ile Ala Thr Thr Asn Ala Val Ile Ala Gly Leu Ile Val Leu  
385 390 395 400

5 Glu Gly Leu Lys Ile Leu Ser Gly Lys Ile Asp Gln Cys Arg Thr Ile  
405 410 415

Phe Leu Asn Lys Gln Pro Asn Pro Arg Lys Lys Leu Leu Val Pro Cys  
420 425 430

10 Ala Leu Asp Pro Pro Asn Pro Asn Cys Tyr Val Cys Ala Ser Lys Pro  
435 440 445

Glu Val Thr Val Arg Leu Asn Val His Lys Val Thr Val Leu Thr Leu  
450 455 460

15 Gln Asp Lys Ile Val Lys Glu Lys Phe Ala Met Val Ala Pro Asp Val  
465 470 475 480

Gln Ile Glu Asp Gly Lys Gly Thr Ile Leu Ile Ser Ser Glu Glu Gly  
20 485 490 495

Glu Thr Glu Ala Asn Asn His Lys Lys Leu Ser Glu Phe Gly Ile Arg  
500 505 510

25 Asn Gly Ser Arg Leu Gln Ala Asp Asp Phe Leu Gln Asp Tyr Thr Leu  
515 520 525

Leu Ile Asn Ile Leu His Ser Glu Asp Leu Gly Lys Asp Val Glu Phe  
30 530 535 540

Glu Val Val Gly Asp Ala Pro Glu Lys Val Gly Xaa Lys Gln Ala Glu  
545 550 555 560

35 Asp Ala Ala Lys Ser Ile Thr Asn Gly Gln Xaa  
565 570

(2) INFORMATION FOR SEQ ID NO: 475:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Gln Val Val Thr Cys Leu Thr Arg Asp Ser Tyr Leu Thr His Cys  
1 5 10 15

50 Phe Leu Gln His Leu Met Val Val Leu Ser Ser Leu Glu Arg Thr Pro  
20 25 30

Ser Pro Glu Pro Val Asp Lys Asp Phe Tyr Ser Glu Phe Gly Asn Lys  
35 40 45

55 Thr Thr Gly Lys Met Glu Asn Tyr Glu Leu Ile His Ser Ser Arg Val  
50 55 60

60 Lys Phe Thr Tyr Pro Ser Glu Glu Glu Ile Gly Asp Leu Thr Phe Thr  
65 70 75 80

Val Ala Gln Lys Met Ala Glu Pro Glu Lys Ala Pro Ala Leu Ser Ile  
85 90 95

5 Leu Leu Tyr Val Gln Ala Phe Gln Val Gly Met Pro Pro Pro Gly Cys  
100 105 110

Cys Arg Gly Pro Leu Arg Pro Lys Thr Leu Leu Leu Thr Ser Ser Glu  
115 120 125

10 Ile Phe Leu Leu Asp Glu Asp Cys Val His Tyr Pro Leu Pro Glu Phe  
130 135 140

Ala Lys Glu Pro Pro Gln Arg Asp Arg Tyr Arg Leu Asp Asp Gly Arg  
145 150 155 160

Arg Val Arg Asp Leu Asp Arg Val Leu Met Gly Tyr Gln Thr Tyr Pro  
165 170 175

20 Gln Pro Ser Pro Ser Ser Ser Met Thr Cys Lys Val Met Thr Ser Trp  
180 185 190

Ala Val Ser Pro Trp Thr Thr Leu Gly Arg Cys Gln Val Ala Arg Leu  
195 200 205

25 Glu Pro Ala Arg Ala Val Lys Ser Ser Gly Arg Cys Leu Ser Pro Val  
210 215 220

Leu Arg Ala Glu Arg Ser Ser Ser Arg Cys Trp Leu Ala Ser Gly Arg  
225 230 235 240

Pro Cys Val Ala Val Ser Cys Leu Ser Ser Ser Pro Ala Ser Pro Gly  
245 250 255

35 His Ser Gln Pro Val Val Ser Ser Leu Thr Pro Thr Gly Ala Gly Gln  
260 265 270

Gln Ala Phe Val Phe Ser Lys Asn Val Leu Ser Ser Leu Trp Tyr Leu  
275 280 285

40 Asn Leu Thr Val Leu Ala Glu Asn Val Asn Met Cys Val Cys Cys Val  
290 295 300

Asn Ser Phe Ser Cys Trp Glu Xaa  
305 310

(2) INFORMATION FOR SEQ ID NO: 476:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Gln His His Leu Trp Ile Leu Leu Leu Cys Leu Gln Thr Trp  
1 5 10 15

60

Pro Glu Ala Ala Gly Lys Asp Ser Glu Ile Phe Thr Val Asn Gly Ile

	20	25	30
	Leu Gly Glu Ser Val Thr Phe Pro Val Asn Ile Gln Glu Pro Arg Gln		
	35	40	45
5	Val Lys Ile Ile Ala Trp Thr Ser Lys Thr Ser Val Ala Tyr Val Thr		
	50	55	60
10	Pro Gly Asp Ser Glu Thr Ala Pro Val Val Thr Val Thr His Arg Asn		
	65	70	75
	Tyr Tyr Glu Arg Ile His Ala Leu Gly Pro Asn Tyr Asn Leu Val Ile		
	85	90	95
15	Ser Asp Leu Arg Met Glu Asp Ala Gly Asp Tyr Lys Ala Asp Ile Asn		
	100	105	110
	Thr Gln Ala Asp Pro Tyr Thr Thr Thr Lys Arg Tyr Asn Leu Gln Ile		
	115	120	125
20	Tyr Arg Arg Leu Gly Lys Pro Lys Ile Thr Gln Ser Leu Met Ala Ser		
	130	135	140
	Val Asn Ser Thr Cys Asn Val Thr Leu Thr Cys Ser Val Glu Lys Glu		
	145	150	155
25	Glu Lys Asn Val Thr Tyr Asn Trp Ser Pro Leu Gly Glu Glu Gly Asn		
	165	170	175
30	Val Leu Gln Ile Phe Gln Thr Pro Glu Asp Gln Glu Leu Thr Tyr Thr		
	180	185	190
	Cys Thr Ala Gln Asn Pro Val Ser Asn Asn Ser Asp Ser Ile Ser Ala		
	195	200	205
35	Arg Gln Leu Cys Ala Asp Ile Ala Met Gly Phe Arg Thr His His Thr		
	210	215	220
	Gly Leu Leu Ser Val Leu Ala Met Phe Phe Leu Leu Val Leu Ile Leu		
	225	230	235
40	Ser Ser Val Phe Leu Phe Arg Leu Phe Lys Arg Arg Gln Asp Ala Ala		
	245	250	255
45	Ser Lys Lys Thr Ile Tyr Thr Tyr Ile Met Ala Ser Arg Asn Thr Gln		
	260	265	270
	Pro Ala Glu Ser Arg Ile Tyr Asp Glu Ile Leu Gln Ser Lys Val Leu		
	275	280	285
50	Pro Ser Lys Glu Glu Pro Val Asn Thr Val Tyr Ser Glu Val Gln Phe		
	290	295	300
	Ala Asp Lys Met Gly Lys Ala Ser Thr Gln Asp Ser Lys Pro Pro Gly		
	305	310	315
55	Thr Ser Ser Tyr Glu Ile Val Ile Xaa		
	325		
60			

## (2) INFORMATION FOR SEQ ID NO: 477:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

5  
 10 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile  
 1 5 10 15  
 Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr  
 20 25 30  
 15 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile  
 35 40 45  
 20 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu  
 50 55 60  
 Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn  
 65 70 75 80  
 25 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro  
 85 90 95  
 Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu  
 100 105 110  
 30 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His  
 115 120 125  
 35 Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr  
 130 135 140  
 Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu  
 145 150 155 160  
 40 Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser  
 165 170 175  
 Ala Xaa

## (2) INFORMATION FOR SEQ ID NO: 478:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

50  
 55 Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val  
 1 5 10 15  
 60 Ile Leu Gly Leu Leu Cys Leu Leu Leu Cys Gly Gly Gly Glu Gly Lys  
 20 25 30

Val Ala Gly Arg Gln Ala Val Thr Ser Asp Gln Gln Ser Val Gly Arg  
 35 40 45

5 Arg Asp Val Tyr  
 50

10 (2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Gln Lys Lys Asn Ser Leu Phe Phe Phe Phe Ala Phe Tyr Tyr Glu  
 1 5 10 15

20 Asn Lys Thr Asn Ala Pro Gly Glu Gly Ser Met Ile Thr Arg Asn Ile  
 20 25 30

25 Lys Glu Tyr Phe Leu Pro Phe Leu Phe Cys Cys Val Glu Ala Ser Ile  
 35 40 45

Ala Ile Asn Lys Leu Asn Tyr Leu His Trp Thr His Phe Gln  
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

40 Met Pro Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser  
 1 5 10 15

Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly  
 20 25

45

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

55 Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg  
 1 5 10 15

Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly  
 20 25 30

60

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg  
 35 40 45  
 5 His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg  
 50 55 60  
 Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala  
 65 70 75 80  
 10 His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val  
 85 90 95  
 Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu  
 100 105 110  
 15 Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val  
 115 120 125  
 Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Xaa Glu Gln  
 130 135 140  
 20 Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met  
 145 150 155 160  
 25 Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro  
 165 170 175  
 Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val  
 180 185 190  
 30 Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr  
 195 200 205  
 35 Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys  
 210 215 220  
 Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp  
 225 230 235 240  
 40 Lys Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe  
 245 250 255  
 Thr Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro  
 260 265 270  
 45 Val Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe  
 275 280 285  
 50 Thr Tyr Val Ser Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln  
 290 295 300  
 Leu Val Pro Glu Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys  
 305 310 315 320  
 55 Gly Arg Tyr Leu Gln Met Lys Ala Lys Xaa Gln Gly His Ala Xaa Xaa  
 325 330 335  
 60 Gln Pro Xaa



## (2) INFORMATION FOR SEQ ID NO: 482:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Leu Asn Ser Asn Ile Asn Asp Leu Leu Met Val Thr Tyr Leu Ala  
1 5 10 15  
Asn Leu Thr Gln Ser Gln Ile Ala Leu Asn Glu Lys Leu Val Asn Leu  
20 25 30

20

## (2) INFORMATION FOR SEQ ID NO: 483:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu  
1 5 10 15  
Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr Arg Ile Gly  
20 25 30  
Cys Phe Lys Thr Ile Thr Cys Trp Pro Thr Ser Leu Thr Gln Arg Xaa  
35 40 45

40

45

## (2) INFORMATION FOR SEQ ID NO: 484:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Tyr Met Tyr Ser Leu Asn Val Phe Leu Ser Phe Ile Phe Leu Ala  
1 5 10 15  
Leu Val Phe Lys Cys Val His Val Cys Gln Gly Ala Asn Ala Phe Leu  
20 25 30  
Phe Leu Lys Leu Val Phe  
35

60

## (2) INFORMATION FOR SEQ ID NO: 485:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Gly Leu Arg Leu Ile Cys Leu Glu Leu Thr Met Val Lys Ala Leu  
 1 5 10 15

15

Val Cys Glu Met Phe Leu Phe Phe Leu Met Thr Gln Lys Leu Ile Trp  
 20 25 30

Gln Glu Cys Thr Glu Lys Phe Ala Lys Leu Leu Val Gln Leu Ile Ser  
 35 40 45

20

Leu Val Phe Ala Trp Glu Phe Phe Ser Glu Asp Thr Pro  
 50 55 60

25

## (2) INFORMATION FOR SEQ ID NO: 486:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val  
 1 5 10 15

35

Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile  
 20 25 30

40

Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys  
 35 40 45

Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu  
 50 55 60

45

Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met  
 65 70 75 80

50

Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu  
 85 90 95

Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys  
 100 105 110

55

Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr  
 115 120 125

Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala  
 130 135 140

60

648

Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp  
 145 150 155 160  
 Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu  
 5 165 170 175  
 Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala  
 180 185 190  
 10 Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr  
 195 200 205  
 Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly  
 210 215 220  
 15 Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys  
 225 230 235 240  
 Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe  
 20 245 250 255  
 Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly  
 260 265 270  
 25 Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser  
 275 280 285  
 Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val  
 290 295 300  
 30 Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu  
 305 310 315 320  
 Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met  
 35 325 330 335  
 Leu Ala Thr Gly Gly Asn Arg Lys Lys Xaa  
 340 345

40

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

50

Met Glu Glu Val Leu Leu Leu Gly Leu Lys Asp Arg Glu Gly Tyr Thr  
 1 5 10 15

Ser Phe Trp Asn Asp Cys Ile Ser Ser Gly Leu Arg Gly Cys Met Leu  
 20 25 30

55

Ile Glu Leu Ala Leu Arg Gly Arg Leu Gln Leu Glu Ala Cys Gly Met  
 35 40 45

60

Arg Arg Lys Ser Leu Leu Thr Arg Lys Val Ile Cys Lys Ser Asp Ala  
 50 55 60

Pro Thr Gly Asp Val Leu Leu Asp Glu Ala Leu Lys His Val Lys Glu  
 65 70 75 80  
 5 Thr Gln Pro Pro Glu Thr Val Gln Asn Trp Ile Glu Leu Leu Ser Gly  
 85 90 95  
 Glu Thr Trp Asn Pro Leu Lys Leu His Tyr Gln Leu Arg Asn Val Arg  
 100 105 110  
 10 Glu Arg Leu Ala Lys Asn Leu Val Glu Lys Gly Val Leu Thr Thr Glu  
 115 120 125  
 Lys Gln Asn Phe Leu Leu Phe Asp Met Thr Thr His Pro Leu Thr Asn  
 130 135 140  
 Asn Asn Ile Lys Gln Arg Leu Ile Lys Lys Val Gln Glu Ala Val Leu  
 145 150 155 160  
 20 Asp Lys Trp Val Asn Asp Pro His Arg Met Asp Arg Arg Leu Leu Ala  
 165 170 175  
 Leu Ile Tyr Leu Ala His Ala Ser Asp Val Leu Glu Asn Ala Phe Ala  
 180 185 190  
 25 Pro Leu Leu Asp Glu Gln Tyr Asp Leu Ala Thr Lys Arg Val Arg Gln  
 195 200 205  
 Leu Leu Asp Leu Asp Pro Glu Val Glu Cys Leu Lys Ala Asn Thr Asn  
 210 215 220  
 Glu Val Leu Trp Ala Val Val Ala Ala Phe Thr Lys Xaa  
 225 230 235

35

(2) INFORMATION FOR SEQ ID NO: 488:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

45

Met Ala Gln Arg Met Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp  
 1 5 10 15

Ile Glu Lys Asp Gln Ile Ile Glu Met Ala Cys Leu Ile Thr Asp Ser  
 20 25 30

50

Asp Leu Asn Ile Leu Ala Glu Gly Pro Asn Leu Ile Ile Lys Gln Pro  
 35 40 45

55

Asp Glu Leu Leu Asp Ser Met Ser Asp Trp Cys Lys Glu His His Gly  
 50 55 60

Lys Ser Gly Leu Thr Lys Ala Val Lys Glu Ser Thr Ile Thr Leu Gln  
 65 70 75 80

60

Gln Ala Glu Tyr Glu Phe Leu Ser Phe Val Arg Gln Gln Thr Pro Pro

650

85 90 95

Gly Leu Cys Pro Leu Ala Gly Asn Ser Val His Glu Asp Lys Lys Phe  
100 105 110

5 Leu Asp Lys Tyr Met Pro Gln Phe Met Lys His Leu His Tyr Arg Ile  
115 120 125

10 Ile Asp Val Ser Thr Val Lys Glu Leu Cys Arg Arg Trp Tyr Pro Glu  
130 135 140

Glu Tyr Glu Phe Ala Pro Lys Lys Ala Ala Ser His Arg Ala Leu Asp  
145 150 155 160

15 Asp Ile Ser Glu Ser Ile Lys Glu Leu Gln Phe Tyr Arg Asn Asn Ile  
165 170 175

Phe Lys Lys Lys Ile Asp Glu Lys Lys Arg Lys Ile Ile Glu Asn Gly  
180 185 190

20 Glu Asn Glu Lys Thr Val Ser Xaa  
195 200

25

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

35 Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly  
1 5 10 15

Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala  
20 25 30

40 Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu  
35 40 45

Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala  
50 55 60

45 Asp Ala Ala Asp Ala Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu  
65 70 75 80

50 Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln  
85 90 95

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr  
100 105 110

55 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln  
115 120 125

Val Arg Thr Gly Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn  
130 135 140

60

651

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val  
 145 150 155 160  
 5 Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr  
 165 170 175  
 Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe  
 180 185 190  
 10 Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu  
 195 200 205  
 Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr  
 210 215 220  
 15 Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His  
 225 230 235 240  
 Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser  
 245 250 255  
 20 Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr  
 260 265 270  
 25 Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe  
 275 280 285  
 Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu  
 290 295 300  
 30 Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg  
 305 310 315 320  
 Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu  
 325 330 335  
 35 Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His Xaa  
 340 345 350  
 40

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

50 Met Arg Gly Ser Arg Gly Gly Trp Ala Gly Glu Met Ala Ala Ser Gly  
 1 5 10 15  
 Glu Ser Gly Thr Ser Gly Gly Gly Gly Ser Thr Glu Glu Ala Phe Met  
 20 25 30  
 55 Thr Phe Tyr Ser Glu Val Lys Gln Ile Glu Lys Arg Asp Ser Val Leu  
 35 40 45  
 60 Thr Ser Lys Asn Gln Ile Glu Arg Leu Thr Arg Pro Gly Ser Ser Tyr  
 50 55 60

652

Phe Asn Leu Asn Pro Phe Glu Val Leu Gln Ile Asp Pro Glu Val Thr  
 65 70 75 80  
 5 Asp Glu Glu Ile Lys Lys Arg Phe Arg Gln Leu Ser Ile Leu Val His  
 85 90 95  
 Pro Asp Lys Asn Gln Asp Asp Ala Asp Arg Ala Gln Lys Ala Phe Glu  
 100 105 110  
 10 Ala Val Asp Lys Ala Tyr Lys Leu Leu Leu Asp Gln Glu Gln Lys Lys  
 115 120 125  
 Arg Ala Leu Asp Val Ile Gln Ala Gly Lys Glu Tyr Val Glu His Thr  
 130 135 140  
 15 Val Lys Glu Arg Lys Lys Gln Leu Lys Lys Glu Gly Lys Pro Thr Ile  
 145 150 155 160  
 20 Val Glu Glu Asp Asp Pro Glu Leu Phe Lys Gln Ala Val Tyr Lys Gln  
 165 170 175  
 Thr Met Lys Leu Phe Ala Glu Leu Glu Ile Lys Arg Lys Glu Arg Glu  
 180 185 190  
 25 Ala Lys Glu Met His Glu Arg Lys Arg Gln Arg Glu Glu Glu Ile Glu  
 195 200 205  
 Ala Gln Glu Lys Ala Lys Arg Glu Arg Glu Trp Gln Lys Asn Phe Glu  
 210 215 220  
 30 Glu Ser Arg Asp Gly Arg Val Asp Ser Trp Arg Asn Phe Gln Ala Asn  
 225 230 235 240  
 35 Thr Lys Gly Lys Lys Glu Lys Lys Asn Arg Thr Phe Leu Arg Pro Pro  
 245 250 255  
 Lys Val Lys Met Glu Gln Arg Glu Xaa  
 260 265  
 40

(2) INFORMATION FOR SEQ ID NO: 491:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

55 Asp Ser Met Pro Thr Cys Pro Leu Xaa Ala Ser Leu Glu Cys Gly Pro  
 1 5 10 15  
 Leu Leu Pro Val Arg Leu Cys Cys Leu  
 20 25

(2) INFORMATION FOR SEQ ID NO: 492:

60

653

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Asn Glu Tyr Arg Val Pro Glu Leu Asn Val Gln Asn Gly Val Leu  
1 5 10 15

10 Lys Ser Leu Ser Phe Leu Phe Glu Tyr Ile Gly Glu Met Gly Lys Asp  
20 25 30

Tyr Ile Tyr Ala Val Thr Pro Leu Leu Glu Asp Ala Leu Met Asp Arg  
35 40 45

15 Asp Leu Val His Arg Gln Thr Ala Ser Ala Val Val Gln His Met Ser  
50 55 60

20 Leu Gly Val Tyr Gly Phe Gly Cys Glu Asp Ser Leu Asn His Leu Leu  
65 70 75 80

Asn Tyr Val Trp Pro Asn Val Phe Glu Thr Ser Pro His Val Ile Gln  
85 90 95

25 Ala Val Met Gly Ala Leu Glu Gly Leu Arg Val Ala Ile Gly Pro Cys  
100 105 110

Arg Met Leu Gln Tyr Cys Leu Gln Gly Leu Phe His Pro Ala Arg Lys  
115 120 125

30 Val Arg Asp Val Tyr Trp Lys Ile Tyr Asn Ser Ile Tyr Ile Gly Ser  
130 135 140

35 Gln Asp Ala Leu Ile Ala His Tyr Pro Arg Ile Tyr Gln Arg Xaa  
145 150 155

## 40 (2) INFORMATION FOR SEQ ID NO: 493:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ile Ser Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met  
1 5 10 15

50 Tyr Asp Gly Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln  
20 25 30

Leu Glu Asp Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala  
35 40 45

55 Ala Lys Glu Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu  
50 55 60

60 Phe Ser Gly Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr  
65 70 75 80



654

Gly Pro Val Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys  
                             85                            90                            95  
 5 Glu Glu Asn Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro  
                             100                            105                            110  
 His Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln  
                             115                            120                            125  
 10 Ala Lys Trp Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys  
                             130                            135                            140  
 Asn Leu Ile Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro  
 15 145                            150                            155                            160  
 Thr Leu Lys Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn  
                             165                            170                            175  
 20 Ser Met Leu Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr  
                             180                            185                            190  
 Leu Leu Val Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile  
                             195                            200                            205  
 25 Trp Ile Ser Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln  
                             210                            215                            220  
 Ala Leu Leu Thr Val Val Ser Gln Val Leu Cys Phe Leu Xaa Ile Glu  
 30 225                            230                            235                            240  
 Trp Tyr Leu Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn  
                             245                            250                            255  
 35 Leu Leu Tyr Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val  
                             260                            265                            270  
 Met Ile Gln Lys Pro Trp Xaa  
                             275

40

(2) INFORMATION FOR SEQ ID NO: 494:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

50

Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro  
 1                            5                            10                            15

55

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly  
 20                            25                            30

Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp  
 35                            40                            45

60

Trp Lys Cys Ser Gln Glu Gly Gly Ser Gly Ser Tyr Glu Glu Gly

655

[illegible]

(2) INFORMATION FOR SEQ ID NO: 495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

40	Met	Ala	Ala	Gly	Asp	Gln	Val	Phe	Ser	Gly	Ala	Gly	His	Val	Xaa	Glu
	1					5					10					15
	His	Val	Ala	Gly	Gly	Arg	His	Ala	Trp	Leu	Leu	Thr	Trp	Gln	Ser	Ala
				20					25					30		
45	Cys	Pro	Ala	Asn	Arg	Leu	Ser	Leu	Val	Pro	Leu	Val	Pro	Ser	Ala	Ser
			35					40					45			
	Met	Thr	Arg	Leu	Met	Arg	Xaa	Arg	Thr	Ala	Ser	Gly	Ser	Ser	Val	Ile
50		50					55					60				
	Leu	Trp	Met	Ala	Pro	Ala	Ala	Ala	Pro	Thr	Pro	Ala	Arg	Ala	Pro	Glu
	65					70					75					80
55	Ala	Ala	Pro	Thr	Pro	Ala	Arg	Ala	Pro	Ala	Ala	Ala	Arg	Thr	Pro	Ala
					85					90					95	
	Arg	Gly	Pro	Thr	Trp	Thr	Ser	Pro	Pro	Thr	Arg	Val	Leu	Leu	Gly	Thr
				100					105						110	

656

Xaa Pro Gly Pro Ser Pro Trp Arg Ser Pro Ala Arg Arg Pro Ala Gln  
115 120 125

5 Leu Pro Pro Pro Asp Ser Asp Leu Cys Ser Gly Pro Leu Leu Pro Gly  
130 135 140

Pro Phe Ser Pro Pro Ala Cys His Thr Ala Pro Asn Ser Val Leu Ile  
145 150 155 160

10 Gln Ser Leu Phe Cys Lys Ser Glu Leu Trp Trp Arg Gln Met Arg Ser  
165 170 175

Ile Thr Trp Val Pro Ser Pro Lys Ala Gly Trp Arg Trp Thr Lys Gly  
180 185 190

15 Arg Lys Gln Ala Ser Pro His Arg Ile Leu Phe His Xaa  
195 200 205

20

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

30 Met Ala Leu Thr Leu Leu Pro Ser Val Ser Arg Leu Pro Gly Glu Arg  
1 5 10 15

Met Ala Ala Ser Gly Leu Pro Tyr Val Leu His His Lys Ser Ser Leu  
20 25 30

35 Met Lys Val Ile Phe Phe Pro Tyr Pro Val Leu Pro Leu Pro Ala Pro  
35 40 45

Asn Gly Thr Trp Val Pro Arg Leu Val Leu Gly Leu Gly Ser Gly Asp  
50 55 60

40

Gln Val His Tyr Leu Pro Ile Ser Ser Ser Ile Val Asn Tyr Gly Thr  
65 70 75 80

45 Ser Val Ser Gly Lys Ser Trp Val Phe Leu Val Tyr Pro Leu His Pro  
85 90 95

Thr Pro Thr Trp Ser Thr Arg Cys Phe Gln Val Trp Asp Leu Leu Ser  
100 105 110

50

Val Glu Leu Pro Asp Lys Gly Glu Gly Asn Thr Arg Arg Ala Ser Gly  
115 120 125

Val Pro Gly Leu Ser Gln Leu Pro Thr Ser His Lys Pro Ile Lys Gln  
130 135 140

55

Glu Tyr Xaa  
145

60

## (2) INFORMATION FOR SEQ ID NO: 497:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val  
 1 5 10 15  
 Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys Glu Val Gly  
 20 25 30  
 Ala Ala Leu Pro Pro Arg Gly Pro Ser Leu Ser Asp Cys Leu Gly Leu  
 35 40 45  
 Pro Pro Trp Thr Pro Trp Gly Pro Ala Trp Thr Leu Ala Gln Ser Xaa  
 50 55 60

## (2) INFORMATION FOR SEQ ID NO: 498:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Met Ser Thr Gly Ala Leu Asn Thr Ser Pro Pro Ala Ser Asn Arg Leu  
 1 5 10 15  
 Glu Ser Thr Leu Asn Glu Tyr Leu Ile Gln Pro Gln Leu His Cys Ser  
 20 25 30  
 Ser Val Gln Arg Leu Thr Leu Lys Trp Gly Cys Ser Ser Leu Gln Arg  
 35 40 45  
 Asp Gly Gln Ala Val Pro Trp Gly Leu Trp Gln Arg Ala Tyr Pro Ser  
 50 55 60  
 Leu Leu Pro Thr Leu Pro Ser Asp Leu Leu Arg Pro His Ala Val Thr  
 65 70 75 80  
 Pro Ser Val Ser Val Ser Val His Thr Cys Glu Ser Ser Xaa  
 85 90

## (2) INFORMATION FOR SEQ ID NO: 499:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

658

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Xaa Leu Phe Ser Ser Ser  
1 5 10 15

5 Leu Pro Phe Leu Trp Leu  
20

10 (2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Arg Gly Gly Leu Cys Pro Leu Leu Val Pro Gly Pro Leu Ala Arg Gln  
1 5 10 15

20 Glu Pro Ser Pro Ser Leu Gln Gly Cys Ser Glu Ser Pro Val Gly Met  
20 25 30

25 Asp

30 (2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu  
1 5 10 15

40 Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser  
20 25

45 (2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Pro Gly Lys Pro Gln Ala Cys Pro Glu Leu Thr Ser Val Leu Pro  
1 5 10 15

55

(2) INFORMATION FOR SEQ ID NO: 503:

60 (i) SEQUENCE CHARACTERISTICS:

659

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

5

Asn Lys Ser Leu Xaa Ser Cys Leu Phe Val Leu His Phe Val Leu His  
1 5 10 15

Cys Xaa Phe

10

(2) INFORMATION FOR SEQ ID NO: 504:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Lys Thr His Arg Leu Arg Ile Arg Asn Pro Cys Leu Gln Phe  
1 5 10 15

25

Ser Ile Leu Asn Leu Phe Leu Leu Lys Met Ile Val Ser  
20 25

30

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln  
1 5 10 15

40

Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu  
20 25 30

45

Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly  
35 40 45

Pro Ser Ser Phe Gln Asn Pro Ala Ser Ser Pro Ser Ser Trp Thr His  
50 55 60

50

Glu Glu Glu Pro Gly Tyr Phe Pro Gln Tyr Xaa  
65 70 75

55

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Leu Pro Leu Ala Glu Leu Lys Asn Trp Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Leu Trp Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu  
1 5 10 15

Ser Asp Thr Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr  
20 25 30

Gly Asp Val Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys  
35 40 45

Thr Gly Val Met Gly Val Cys Cys Thr Ala Leu Val Ala Val Val  
50 55 60

Ala Arg Lys Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe  
65 70 75 80

Met Met Asp Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg  
85 90 95

Val Leu Gln Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu  
100 105 110

Ser His Ala Ala Arg Arg His Gln Arg Xaa Leu Leu Ala Ala Ile Asn  
115 120 125

Ala Phe Arg Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val  
130 135 140

Asn Ser Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu  
145 150 155 160

Gln Gln Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp  
165 170 175

Thr Leu Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala  
180 185 190

Leu Gly Pro Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa  
195 200 205

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

661

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

5 Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val  
1 5 10 15

Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Ala Pro Ala  
20 25 30

10

Val Xaa Lys Lys  
35

15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

25 Met Ala Leu Val Ala Leu Phe Thr Gln Leu Met Arg Xaa Leu Gly Arg  
1 5 10 15

Cys Pro Gln

30

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

40 Met Thr Phe Pro Phe Glu Lys Glu Asn Ser Cys Phe Gln Cys Leu Leu  
1 5 10 15

Phe Asp Ser Trp Arg Glu Gln Thr Arg Thr Asn Ile Gln Pro Gln Arg  
20 25 30

45

50

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

60 Met His Leu Leu Asp Phe Phe Arg Asp Leu Val Leu Leu Val Leu Leu  
1 5 10 15



Ala Leu Leu Asp Ser Phe Trp Leu Glu Val Gln Lys  
20 25

5

(2) INFORMATION FOR SEQ ID NO: 512:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

10

15 Met Cys Leu Ile His Phe Ile Lys Ile Ile Leu Val Phe Ile Leu Lys  
1 5 10 15

Leu Trp Leu Tyr Ser Gln Lys Cys Pro Lys  
20 25

20

(2) INFORMATION FOR SEQ ID NO: 513:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

25

30 Met Ile His Val His Glu Trp Asn Asp Gln Met Leu Met Val Tyr Ile  
1 5 10 15

35 Phe Leu Tyr Pro Val Ser Ile Thr Phe Leu Asn Leu Cys Ser Leu Thr  
20 25 30

Cys

40

(2) INFORMATION FOR SEQ ID NO: 514:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

45

50 Leu Asn Glu Ser Tyr Val Ser Arg Ala Gly Gly Trp Phe Ser Met Phe  
1 5 10 15

Xaa Leu Ile Phe Phe Leu Leu Ala Leu Gly Ser Xaa Leu Cys Leu Leu  
20 25 30

55

Leu Cys Leu Pro Ser Phe Asn Lys Thr Arg Arg Lys Gln Lys Pro  
35 40 45

60

## (2) INFORMATION FOR SEQ ID NO: 515:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Ser Ser Lys Thr Pro Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly Ser  
 1 5 10 15

Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu Gly  
 20 25 30

Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp  
 35 40

## (2) INFORMATION FOR SEQ ID NO: 516:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Leu Asn Trp  
 1

## (2) INFORMATION FOR SEQ ID NO: 517:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Phe Ala Phe Cys Ala Glu Leu Met Ile Gln Asn Trp Thr Leu Gly Ala  
 1 5 10 15

Val Asp Ser Gln Met Asp Asp Met Asp Met Asp Leu Asp Lys Glu Phe  
 20 25 30

Leu Gln Asp Leu Lys Glu Leu Lys Val Leu Val Ala Asp Lys Asp Leu  
 35 40 45

Leu Asp Leu His Lys Ser Leu Val Cys Thr Ala Leu Arg Gly Lys Leu  
 50 55 60

Gly Val Phe Ser Glu Met Glu Ala Asn Phe Lys Asn Leu Ser Arg Gly  
 65 70 75 80

Leu Val Asn Val Ala Lys Leu Thr His Asn Lys Asp Val Arg Asp  
 85 90 95

Leu Phe Val Asp Leu Val Glu Lys Phe Val Glu Pro Cys Arg Ser Asp  
 100 105 110

His Trp Pro Leu Ser Asp Val Arg Phe Phe Leu Asn Gln Tyr Ser Ala  
115 120 125

5 Ser Val His Ser Leu Asp Gly Phe Arg His Gln Ala Ser Gly Thr Ala  
130 135 140

Thr Trp Ala Pro Ser Ala Ala Ala Ser Cys Ala Cys Ile Met Thr Glu  
145 150 155 160

10

Val Pro Pro Asn Ala Pro Pro Thr Leu Thr Ile Lys Leu Leu  
165 170

15

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

20

25 Met Trp Lys Asn Leu Gly Ser Gly Ser Val Phe Val Thr Trp Phe Ser  
1 5 10 15

Leu Val Met Ile Leu Ser Gly Ile Gly Pro Leu Gly Asp Ala Glu Asp  
20 25 30

30

Ser Ile Ser Asp Val Ser His Arg Leu Arg Pro  
35 40

35

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

40

Phe Gln Phe Pro Leu Leu Thr Ile Ala Leu Gln Phe Leu  
1 5 10

45

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

50

55 Met His Tyr Val Ile Val Leu Ser Leu Phe Val Val Leu Glu Lys Lys  
1 5 10 15

55

60 Asn Lys Met Gly Ser Asp Gly Cys Leu Arg Lys Asn Gly Ser  
20 25 30

60

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Arg Ser Ile Val Leu Arg Gly Ser Leu Phe Leu Phe Phe Ser  
 1 5 10 15  
 His Tyr Thr Leu Lys Leu Leu Ser Val Ile Lys Gln Thr Asn Arg Lys  
 20 25 30  
 Ile Val Trp Glu Lys Pro Cys Ile Arg Leu Phe Tyr Xaa Val Leu  
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Leu Pro Val Leu Leu Cys Leu Thr Leu Pro Met Pro Leu Pro  
 1 5 10 15  
 Ser Ala Thr Ala Arg Gly Gly Asn Arg Thr  
 20 25

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Ser Ser Ile Pro Val Ser Ile Leu Ile Gly Met Lys Leu Ile Leu Tyr  
 1 5 10 15  
 Leu Leu Ile Thr Glu Ser Gly Ser His Glu Lys Lys Ser Phe Tyr Pro  
 20 25 30  
 Ser Phe Lys Tyr Met Phe Lys Ile Ile Ile Tyr Val Ser Ala Tyr Cys  
 35 40 45  
 Arg Thr Ala Leu Arg Ala Thr Val Ser His  
 50 55

666

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Asn Arg Thr Leu Leu Phe Leu Ile Leu Phe Val Leu Phe Gly Leu Gly  
 1 5 10 15

Tyr Gly Phe

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Phe Leu Leu Val Leu Ser Val Phe Cys Asp Phe Met Cys Ser Ile  
 1 5 10 15

Ala Pro Arg Cys His Ala Leu Ser Leu Val Ser Leu Arg Ala Gln His  
 20 25 30

Leu Ser Leu Phe Ile Thr Cys His  
 35 40

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Leu Leu Phe Ile Leu Leu Thr Leu Ser Ser Gly Cys Arg Leu Leu  
 1 5 10 15

Val Ser Ser Trp Lys Thr Phe Leu Pro His Phe Ser Leu Pro Gly Pro  
 20 25 30

Arg Glu His Pro Glu Gly Ser Arg Thr Trp Phe Phe Arg Tyr Trp Glu  
 35 40 45

Pro Gly Ala His Cys Leu His Cys Ala  
 50 55

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

5

Ala Arg Leu Leu Leu Phe Leu Ser Ser Val His Pro Ser Ile Met Pro  
 1 5 10 15

10

Ser Cys Asn Gln Leu  
 20

15

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Ser Leu Thr Ser Ser Leu Thr Phe Leu Ser His Ile Leu Leu Leu  
 1 5 10 15

25

Pro Gln Lys Leu Gln Phe Leu Ser Trp Met Glu Arg Gln Gln Arg Cys  
 20 25 30

30

Thr Gly Val Ala Lys Tyr Ala  
 35

35

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

Met Val Leu Arg Leu Ile Gln Leu Ile Phe Leu Ile Phe Phe Ile His  
 1 5 10 15

45

Ile Ile Ile Leu Leu Ile Pro Gly Ser Arg Pro Cys Gly Ser Trp Val  
 20 25 30

Asn Asp Arg Xaa Leu Gly Leu Arg Asp Val Thr His Leu Ile Tyr Leu  
 35 40 45

50

His Trp Val His Gly His Leu Pro Trp Cys His Pro Tyr Ile Gln Val  
 50 55 60

55

Glu Phe Ser Ala Leu Ile Glu Ser Thr Ala Gln Leu Gly Leu Pro Phe  
 65 70 75 80

Ser Trp Val Arg Val Ile His Pro Phe Leu Val Leu Pro Cys Leu Tyr  
 85 90 95

60

Ser Pro Gly Leu Lys Asn Gly Ile Phe Leu Phe Leu Leu Arg Ala Met  
 100 105 110

Pro Gly Gly Met Phe Pro Gly Asn Leu Glu Ala Phe Arg Val Pro Val  
 115 120 125

5

## 10 (2) INFORMATION FOR SEQ ID NO: 530:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser  
 1 5 10 15

20

Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe  
 20 25 30

25

Trp Gly Phe Gly Xaa Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr  
 35 40 45

Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser  
 50 55 60

30

His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln  
 65 70 75 80

Pro Asn

35

## (2) INFORMATION FOR SEQ ID NO: 531:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala  
 1 5 10 15

50

Tyr Trp Thr Met  
 20

55

## (2) INFORMATION FOR SEQ ID NO: 532:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

669

Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln Leu Lys Ile  
1 5 10 15

5 Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu Lys Ile Ile  
20 25 30

Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser Trp Ala Ile  
35 40 45

10 Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn Lys Thr Ala  
50 55 60

15 Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr  
65 70 75

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser  
1 5 10 15

30 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Xaa Ser Tyr Leu Trp  
20 25 30

Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Xaa Trp Ala Cys  
35 40 45

35 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe  
1 5 10 15

Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg  
20 25 30

55 Ile Leu Phe Phe Ile Val Phe  
35

(2) INFORMATION FOR SEQ ID NO: 535:



670

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Leu

1

## (2) INFORMATION FOR SEQ ID NO: 536:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Asp Gln Phe Lys Ile Phe Tyr Phe Leu Lys Ala Phe Phe Ala Cys  
1 5 10 15

Cys Asn Val Gln Asp Pro Ser Pro Phe Met Gly Glu Thr Gly Ser Tyr  
20 25 30

Leu Asn Ile Gly  
35

## (2) INFORMATION FOR SEQ ID NO: 537:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Phe Asp Phe Leu Ser Tyr Phe Lys Asp Leu Leu Ser Cys  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 538:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Gly Phe Gly Phe Val Leu Asn Ile Phe Ser Phe Phe Leu Xaa Pro  
1 5 10 15

Pro Leu

## (2) INFORMATION FOR SEQ ID NO: 539:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

Leu Leu Leu Trp Thr Leu Leu Ala Xaa Tyr Xaa  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 540:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu  
1 5 10 15

Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg  
20 25 30

Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe  
35 40 45

Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys  
50 55 60

Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe  
65 70 75 80

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu  
85 90 95

Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Xaa  
100 105

## (2) INFORMATION FOR SEQ ID NO: 541:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Phe Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met  
1 5 10 15

Leu Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr  
20 25 30

Leu Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser  
35 40 45

Pro Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe  
50 55 60

5 Trp Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr  
65 70 75 80

Leu Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val  
85 90 95

10

Asp Gly Glu Glu Leu Gln Met Glu Pro Val  
100 105

15

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

20

25 Met Asp Arg Phe Thr Val Ala Gly Val Leu Pro Asp Ile Glu Gln Phe  
1 5 10 15

Phe Asn Ile Gly Asp Ser Ser Ser Gly Leu Ile Gln Thr Val Phe Ile  
20 25 30

30

Ser Ser Tyr Met Val Leu Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg  
35 40 45

Tyr Asn Arg Lys Tyr Leu Met Cys Gly Gly Ile Ala Phe Trp Ser Leu  
50 55 60

35

Val Thr Leu Gly Ser Ser Phe Ile Pro Gly Glu His Phe Trp Leu Leu  
65 70 75 80

40

Leu Leu Thr Arg Gly Leu Val Gly Val Gly Glu Ala Ser Tyr Ser Thr  
85 90 95

Ile Ala Pro Thr Leu Ile Ala Asp Leu Phe Val Ala Asp Gln Arg Thr  
100 105 110

45

Gly Cys Ser Ala Ser Ser Thr Leu Pro Phe Arg Trp Ala Val Val Trp  
115 120 125

Ala Thr Leu Gln Ala Pro Lys Xaa  
130 135

50

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

55

60

673

Met Ala Gly Asp Trp His Trp Ala Leu Arg Val Thr Pro Gly Leu Gly  
 1 5 10 15  
 Val Val Ala Val Leu Leu Leu Phe Leu Val Val Arg Glu Pro Pro Arg  
 5 20 25 30  
 Gly Ala Val Glu Arg His Ser Asp Leu Pro Pro Leu Asn Pro Thr Ser  
 35 40 45  
 10 Trp Trp Ala Asp Leu Arg Ala Leu Ala Arg Asn Pro Ser Phe Val Leu  
 50 55 60  
 Ser Ser Leu Gly Phe Thr Ala Val Ala Phe Val Thr Gly Ser Leu Ala  
 65 70 75 80  
 15 Leu Trp Ala Pro Ala Phe Leu Leu Arg Ser Arg Val Val Leu Gly Glu  
 85 90 95  
 Thr Pro Pro Cys Leu Pro Gly Asp Ser Cys Ser Ser Ser Asp Ser Leu  
 20 100 105 110  
 Ile Phe Gly Leu Ile Thr Cys Leu Thr Gly Val Leu Gly Val Gly Leu  
 115 120 125  
 25 Gly Val Glu Ile Ser Arg Arg Xaa Arg His Ser Asn Pro Arg Ala Asp  
 130 135 140  
 Pro Leu Val Cys Ala Thr Gly Leu Leu Gly Ser Ala Pro Phe Leu Phe  
 145 150 155 160  
 30 Leu Ser Leu Ala Cys Ala Arg Gly Ser Ile Val Ala Thr Tyr Ile Phe  
 165 170 175  
 Ile Phe Ile Gly Glu Thr Leu Leu Ser Met Asn Trp Ala Ile Val Ala  
 35 180 185 190  
 Asp Ile Leu Leu Tyr Val Val Ile Pro Thr Arg Arg Ser Thr Ala Glu  
 195 200 205  
 40 Ala Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala Gly Ser Pro  
 210 215 220  
 Tyr Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn Trp Pro Pro  
 225 230 235 240  
 45 Ser Phe Leu Ser Glu Phe Arg Ala Leu Gln Phe Ser Leu Met Leu Cys  
 245 250 255  
 Ala Phe Val Gly Ala Leu Gly Gly Ala Leu Ser Trp Ala Pro Xaa Ser  
 50 260 265 270  
 Ser Leu Arg Pro Thr Ala Gly Gly His Ser Cys Thr Cys Arg Ala Cys  
 275 280 285  
 55 Cys Thr Lys Gln Gly Pro Gln Thr Thr Gly Leu Trp Cys Pro Ser Gly  
 290 295 300  
 Ala Ala Pro Pro Ala Cys Pro Trp Pro Val Cys Ser Ser Glu Arg Leu  
 305 310 315 320  
 60

Pro Leu Thr Tyr Leu His Ile Cys His Ser Xaa Pro Trp Ala His Pro  
 325 330 335

5 Thr Lys Gly Leu Gly Leu Thr Pro Trp Pro Gly Pro Ala Ser Arg Gly  
 340 345 350

Thr Leu Gly Arg Val Pro Ala Pro Arg His Tyr Xaa Gly Ser Ser Gly  
 355 360 365

10 Glu Glu Val Gly Val Gln Glu Gly Asp Pro Ser Pro Gln Gly Xaa Pro  
 370 375 380

Gln Gly Leu Gly Ala Ile Cys Asn Gly Ile Lys Phe Val Ala Arg Pro  
 385 390 395 400

15 Gln Val Pro Ala Leu Val Phe Leu Trp Val Ala Ser Asp Leu Ala Pro  
 405 410 415

20 Arg Leu His Pro Arg Ala Pro Glu  
 420

## (2) INFORMATION FOR SEQ ID NO: 544:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Phe Arg Phe Val Ile Cys Leu Phe Leu Trp Leu Val Leu Cys Arg  
 1 5 10 15

35 Asp Ser Thr Ser Ala Ser Arg Ile Ala Leu Tyr Tyr Arg Ile Val Phe  
 20 25 30

Leu Ile His Gln Cys Ser Ser  
 35

40

## (2) INFORMATION FOR SEQ ID NO: 545:

45

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Pro Trp Xaa Ala Gln Leu Leu Asp Arg Thr Ile Gly Pro Leu  
 1 5 10 15

55 Tyr Leu Leu Phe Val Gln Phe Ser Pro Ala Phe Ser Arg Thr Ser Pro  
 20 25 30

Trp Arg Ser Pro Lys Asn Phe Arg Arg Leu Tyr Pro Pro Cys Thr Thr  
 35 40 45

60 Ser Gly Cys Ala Ala Arg Trp Leu Phe Ser

50

55

## 5 (2) INFORMATION FOR SEQ ID NO: 546:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Gly Leu Ser Val Leu Leu Pro Leu Cys Leu Leu Gly Pro Gly Arg  
 1 5 10 15

15

Phe Thr Ser Gly Gln Lys Pro Leu Asp Thr Pro Gly Leu Gly Val Pro  
 20 25 30

Phe

20

## 25 (2) INFORMATION FOR SEQ ID NO: 547:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu  
 1 5 10 15

35

Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr  
 20 25 30

Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu  
 35 40 45

40

Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe  
 50 55 60

Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr  
 65 70 75 80

45

Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala  
 85 90 95

Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr  
 100 105 110

50

Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln  
 115 120 125

55

Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala  
 130 135 140

Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu  
 145 150 155 160

60

676

Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly  
                           165                          170                          175  
 5 Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu  
                           180                          185                          190  
 Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val  
                           195                          200                          205  
 10 Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu  
                           210                          215                          220  
 Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val  
 15 225                          230                          235                          240  
 Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys  
                           245                          250                          255  
 20 Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser  
                           260                          265                          270  
 Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn  
 25 275                          280                          285  
 Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp  
                           290                          295                          300  
 Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe  
 30 305                          310                          315                          320  
 Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp  
                           325                          330                          335  
 35 Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu  
                           340                          345                          350  
 Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln  
 40 355                          360                          365

(2) INFORMATION FOR SEQ ID NO: 548:

45 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 77 amino acids  
       (B) TYPE: amino acid  
       (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:  
 50 Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met  
     1                          5                          10                          15  
 55 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr  
           20                          25                          30  
 Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala  
     35                          40                          45  
 60 Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro

677

50                      55                      60  
 Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu  
 65                      70                      75

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser  
 1                      5                      10                      15  
 His Cys Trp Gly Leu Pro Leu Ala Cys Gly Thr Phe Val Gln Gly His  
 20                      25                      30  
 Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala  
 35                      40                      45

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met Leu Leu Ser Leu Ala Ala Phe Ser Val Ile Ser Val Val Ser Tyr  
 1                      5                      10                      15  
 Leu Ile Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys  
 20                      25                      30  
 Ser Val Ile Gln Ala Val Gln Lys Ser Glu Glu Gly His Pro Phe Lys  
 35                      40                      45  
 Ala Tyr Leu Asp Val Asp Ile Thr Leu Ser Ser Glu Ala Phe His Asn  
 50                      55                      60  
 Tyr Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile  
 65                      70                      75                      80  
 Ile Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala  
 85                      90                      95  
 Val Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile  
 100                      105                      110  
 Thr Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val  
 115                      120                      125  
 Tyr Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg  
 130                      135                      140



Asp Gln Thr Lys Ser Ile Val Glu Lys Ile Gln Ala Lys Leu Pro Gly  
145 150 155 160

5 Ile Ala Lys Lys Lys Ala Glu Xaa  
165

10 (2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Ser Val Pro Phe His Leu Leu Val Val Leu Arg Ser Arg Ala Val Arg  
1 5 10 15

Ala Arg Arg Arg Arg Glu Pro Arg Ser Leu Pro Arg Pro Gly Asp Glu  
20 25 30

Glu Leu Gln Leu Leu Leu Cys Gly Ala Arg Ser Asp Phe Leu Glu Arg  
35 40 45

Cys Glu Glu Asp Trp Val Cys Leu Trp His His Ala Asp His Ala Ala  
50 55 60

Phe Pro Gly Ser Phe Gln Cys His Gln Cys Gly Phe Leu Pro His Pro  
65 70 75 80

Gly Ser Ser Leu Cys His His Gln Leu Gln Asp Leu Gln Val Arg His  
85 90 95

Pro Ser Cys Thr Glu Val Arg Arg Arg Pro Ser Ile Gln Ser Leu Pro  
100 105 110

Gly Arg Arg His Tyr Ser Val Leu Arg Ser Phe Pro  
115 120

45 (2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Val His Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp  
1 5 10 15

Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His  
20 25 30

Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile  
35 40 45

60

679

Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His  
 50 55 60  
 5 Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu  
 65 70 75 80  
 Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro  
 85 90 95  
 10 Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg  
 100 105 110  
 Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr  
 115 120 125  
 15 Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn  
 130 135 140  
 Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val  
 145 150 155 160  
 Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser  
 165 170 175  
 25 Leu

30 (2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu  
 1 5 10 15  
 40 Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His  
 20 25 30  
 45 Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys  
 35 40 45  
 Thr Glu Gly Ile Pro Cys Ala Lys Ile Pro Glu Trp Val Thr His Leu  
 50 55 60  
 50 Thr Trp Gln Thr Leu Lys Asn Ser  
 65 70

55 (2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

5 Val Leu Arg Ile Ile Cys Leu Trp Pro Cys Gly Thr Thr Leu Pro Leu  
1 5 10 15

Val Glu Lys Ala His Asp Ser His Ser Ala Asp Pro Val Cys Pro Gly  
20 25 30

10 Leu Thr Ala His Leu Pro Val Leu Leu Tyr Val Gln Leu  
35 40 45

(2) INFORMATION FOR SEQ ID NO: 555:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Lys His Ala Asp Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser  
1 5 10 15

25 Pro Leu Leu Met Thr Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu  
20 25 30

Ser Leu Gly Pro Arg Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg  
35 40 45

30 Gly Phe Met Ile Val Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr  
50 55 60

Ile Val Tyr Glu Phe Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp  
35 65 70 75 80

Arg Cys Asp Pro Gln Asp Cys Thr Leu Gly Gln Cys Pro Ser Val Pro  
85 90 95

40 Ser Pro Xaa Thr Pro Val Thr Lys Ala Tyr Val Val Arg Thr Glu Gln  
100 105 110

Gly Thr Gly Pro Pro Leu Pro Thr Ala Ala Leu Gln Gly Pro Arg Leu  
115 120 125

45 Trp Phe Leu Thr His Phe Pro Arg Ala Ala Pro Gly Met Trp Pro His  
130 135 140

Cys Cys Leu Pro Leu Gln Ser Trp Gly Leu Lys Gly Leu Tyr Ser Tyr  
50 145 150 155 160

Phe Pro Leu Pro Ala Leu Lys Leu Gly Arg Gly Ala Leu Arg Ala Gly  
165 170 175

55 Pro Thr Lys Gly Leu Val Ala Phe Phe Leu Thr Gln Lys Arg Ser Ala  
180 185 190

Ile Met Ser Leu Trp Thr Gln Ser His Ser Ser Thr Pro His Thr Glu  
195 200 205

60

681

Ala Val Ala Ser Gly Pro Lys Val Arg Val Gly Gly Gly Leu Gly Ile  
210 215 220

5 Gln Pro Val Glu Ala Ala Tyr Ser Thr Cys Val Leu Ile Lys Ser Asp  
225 230 235 240

Arg Gly Asn His Glu Lys Lys Lys Lys Lys  
245 250

10

(2) INFORMATION FOR SEQ ID NO: 556:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

20 Gly Leu Ala Gly Leu Cys Gly Gln Leu Ser Ser Pro Ala Leu Cys Val  
1 5 10 15

Asn Arg Leu

25

(2) INFORMATION FOR SEQ ID NO: 557:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 217 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

35 Met Ile Thr Glu Lys Trp Gly Leu Asn Met Glu Tyr Cys Arg Gly Gln  
1 5 10 15

40 Ala Tyr Ile Xaa Ser Ser Gly Phe Ser Ser Lys Met Lys Val Val Ala  
20 25 30

Ser Arg Leu Leu Glu Lys Tyr Pro Gln Ala Ile Tyr Thr Leu Cys Ser  
35 40 45

45 Ser Cys Ala Leu Asn Met Trp Leu Ala Lys Ser Val Pro Val Met Gly  
50 55 60

Val Ser Val Ala Leu Gly Thr Ile Glu Glu Val Cys Ser Phe Phe His  
65 70 75 80

50

Arg Ser Pro Gln Leu Leu Leu Glu Leu Asp Asn Val Ile Ser Val Leu  
85 90 95

55 Phe Gln Asn Ser Lys Glu Arg Gly Lys Glu Leu Lys Glu Ile Cys His  
100 105 110

Ser Gln Trp Thr Gly Arg His Asp Ala Phe Glu Ile Leu Val Glu Leu  
115 120 125

60

Leu Gln Ala Leu Val Leu Cys Leu Asp Gly Ile Asn Ser Asp Thr Asn

130                      135                      140

Ile Arg Trp Asn Asn Tyr Ile Ala Gly Arg Ala Phe Val Leu Cys Ser  
 145                      150                      155                      160

5 Ala Val Ser Asp Phe Asp Phe Ile Val Thr Ile Val Val Leu Lys Asn  
                     165                      170                      175

10 Val Leu Ser Phe Thr Arg Ala Phe Gly Lys Asn Leu Gln Gly Gln Thr  
                     180                      185                      190

Ser Asp Val Phe Phe Ala Ala Gly Ser Leu Thr Ala Val Leu His Ser  
                     195                      200                      205

15 Leu Asn Glu Val Ile Gly Lys Tyr Xaa  
                     210                      215

20 (2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu Asn Glu  
 1                      5                      10                      15

30 Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg Asn Thr  
                     20                      25                      30

Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile Asn Phe  
 35                      35                      40                      45

Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile Lys Leu  
                     50                      55                      60

40 Tyr Thr Ser Lys Ser Glu Leu Pro Thr Asp Asn Ser Glu Thr Val Glu  
                     65                      70                      75                      80

Asn Thr

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Val Leu Ile Leu Leu Asn Leu Leu Leu Gly Gln Phe Ser Cys Met  
 1                      5                      10                      15

60 Ser Pro Ala Ser His His Cys His Pro Leu Pro Thr Glu Met Pro Cys  
                     20                      25                      30

683

Ser Ser Asp Trp Gly Phe Asp Ser His Thr Val Tyr Pro Ser Cys Val  
 35 40 45

5 Asp Ala Leu Leu Pro Lys Pro Ser Ala Asn Ser Phe Pro Asn Gly Ser  
 50 55 60

Cys His Cys Gln Gly Leu Tyr Asn Gln Gln Gln Gln Asn Leu His Ala  
 65 70 75 80

10 Ala Glu Gly Pro Ala Ser Leu Arg Cys Asn Lys Tyr Val Ser Thr  
 85 90 95

15

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

20 Met Ile Pro Ala Tyr Ser Lys Asn Arg Ala Tyr Ala Ile Phe Phe Ile  
 25 1 5 10 15

Val Phe Thr Val Ile Gly Asp Ala Pro Gly Ala Val Leu Ser Cys Ala  
 20 25 30

30 Gly His Pro Cys Val Gly Phe Ala Ala Val Leu Val Ala Pro Leu Thr  
 35 40 45

Val Ala Val Ser Ser Xaa  
 50

35

(2) INFORMATION FOR SEQ ID NO: 561:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

45 Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu  
 1 5 10 15

50 Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser  
 20 25 30

Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro  
 35 40 45

55 Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys  
 50 55 60

Asp Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu  
 65 70 75 80

60

684

Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg Ile  
85 90 95

5 Asn Val Gly Leu Arg Gly Trp Trp Leu Val Ala Xaa  
100 105

10 (2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys  
1 5 10 15

20 Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala  
20 25 30

Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg  
35 40 45

25 Ala Pro  
50

30

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu  
1 5 10 15

Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu  
20 25 30

45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp  
35 40 45

Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr  
50 55 60

Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu  
65 70 75 80

55 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu  
85 90 95

Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg  
100 105 110

60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

685

115                      120                      125  
 Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg  
 130                      135                      140  
 5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Leu Glu Asp Arg  
 145                      150                      155                      160  
 10 Lys Tyr Glu Tyr Leu Met Thr Leu His Gly Val Val Asn Glu Ser Thr  
 165                      170                      175  
 Val Cys Leu Met Gly His Glu Arg Arg Gln Thr Leu Asn Leu Ile Thr  
 180                      185                      190  
 15 Met Leu Ala Ile Arg Val Leu Ala Asp Gln Asn Val Ile Pro Asn Val  
 195                      200                      205  
 Ala Asn Val Thr Cys Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala  
 210                      215                      220  
 20 Asn Phe Ser Asn Tyr Tyr Ile Ala Gln Val Gln Pro Val Phe Thr Cys  
 225                      230                      235                      240  
 25 Gln Gln Gln Thr Tyr Ser Thr Trp Leu Pro Cys Asn Xaa  
 245                      250

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Ser Phe Leu Met Trp Leu Met Ser Leu Ala Ile Thr Ser Gln Pro  
 1                      5                      10                      15

Pro Met

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe  
 1                      5                      10                      15

Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly  
 20                      25                      30

Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser  
 35                      40                      45



686

Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr  
 50 55 60

5 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Phe  
 65 70 75 80

10

(2) INFORMATION FOR SEQ ID NO: 566:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

20

His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln Val Leu Ser  
 1 5 10 15

25

Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu Ala Pro Gly Arg  
 20 25 30

Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro Trp Phe Thr Ala  
 35 40 45

30

Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys Arg Gln Arg Arg  
 50 55 60

Gln Glu Arg Arg Gln Met Lys Arg Leu  
 65 70

35

(2) INFORMATION FOR SEQ ID NO: 567:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

45

Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys Lys Glu Glu Val Ile  
 1 5 10 15

50

Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp Val Tyr Tyr Phe Ser  
 20 25 30

Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln Leu Ala Arg Tyr Leu  
 35 40 45

55

Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe Arg Thr Gly Lys Met  
 50 55 60

Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn Asp Pro  
 65 70 75 80

60

687

Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu Pro Ile  
                             85                            90                            95  
 5 Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val Thr Asn  
                             100                            105                            110  
 His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn Glu Gln  
                             115                            120                            125  
 10 Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser Ala Ser  
                             130                            135                            140  
 Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys Gly Leu  
 15 145                            150                            155                            160  
 Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser Ala Val  
                             165                            170                            175  
 20 Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln Val Ser  
                             180                            185                            190  
 Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser Gln Pro  
                             195                            200                            205  
 25 Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys Gln Glu  
                             210                            215                            220  
 Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu Met Ala  
 30 225                            230                            235                            240  
 Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile Glu Met  
                             245                            250                            255  
 35 Asp Ser Gly Asp Glu Ala Xaa  
                             260

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Met Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala  
   1                            5                            10                            15  
 50 Leu Arg Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Leu  
                             20                            25                            30  
 Leu Phe Gly Leu Thr His Leu Asn Pro Ser Ala Lys Leu Leu Leu Ser  
                             35                            40                            45  
 55 Gln Met Lys Thr Ser Gly Asn Arg Lys Ser Glu Tyr Ser Lys Tyr Ala  
                             50                            55                            60  
 60 Arg Asn Trp Lys Lys His  
   65                            70

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Pro Val Thr Ser Lys Arg Thr Leu Phe Phe Pro Asp Pro Cys Ser  
1 5 10 15

Tyr Asp Thr Pro Pro Pro Asp Cys His Cys His Ser Phe Arg Ala Glu  
20 25 30

Leu Leu

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu  
1 5 10 15

Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala  
20 25 30

Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu  
35 40 45

His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ser  
50 55 60

Lys Ala Pro Asn Ser Leu Gly Thr Thr Gly Leu Trp Ser Thr Val Tyr  
65 70 75 80

Ile Phe Thr Glu Val Phe His Asn Phe Ser Asn Asn Ser Ile Phe Ser  
85 90 95

Gly Lys Phe Leu Tyr Glu Val Xaa  
100

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

689

Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu Leu His Ile Val Leu  
 1 5 10 15

5 Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala Trp Thr Leu Thr Asn  
 20 25 30

Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu His Ala Val Lys Gly  
 35 40 45

10 Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His  
 50 55 60

15 Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr Ser Ser Arg Lys Phe  
 65 70 75 80

Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu Ala Ser Phe Tyr Thr  
 85 90 95

20 Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr Ala Ser Leu Leu Ser  
 100 105 110

Val Leu Ile Pro Lys Met Pro Gln Leu His Gly Val Arg Ile Phe Gly  
 115 120 125

25 Ile Asn Lys Tyr  
 130

30

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

40 Met Asn Lys Trp Ile Cys Glu Met His Cys Tyr Leu Val Leu Leu Ser  
 1 5 10 15

Val Cys Ser Pro Ser Ala Leu Arg Arg Val Arg His Thr Leu Ser Arg  
 20 25 30

45

50

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

60 Met Pro Val Leu Ser Leu Leu Cys Thr Leu Ile Val Ser Phe Gln Ser  
 1 5 10 15

Ala Asp Ser Cys Glu Val Phe Leu Asn Cys Ser Leu  
20 25

5

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

Met Lys Val Ser Thr Met Leu Trp Phe Leu Cys Trp Glu Gln Ser His  
1 5 10 15

Phe Leu Arg Glu Trp Glu Asp Leu Ser Thr Phe Leu Ile Leu Ile Gln  
20 25 30

Met Glu Cys Gln Tyr Gly Asn Ser  
35 40

25

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser  
1 5 10 15

35

Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Xaa Leu  
20 25 30

40

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

Met Lys Arg Gly Cys Leu Gly Leu Leu Phe Phe Ser Cys Cys Ser Ser  
1 5 10 15

50

Ala Pro Thr Met Leu Leu Cys Asp Tyr Leu Asn Trp Phe  
20 25

55

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

60

691

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

5 Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser Val  
 1 5 10 15

Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu Leu  
 20 25 30

10 Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu Lys  
 35 40 45

Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val Lys  
 15 50 55 60

Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Xaa Asn Arg Arg Arg  
 65 70 75 80

20 Xaa Val Arg Gly Leu Pro Ser Xaa Leu Thr Asn Ser  
 85 90

25 (2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg  
 1 5 10 15

35 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg  
 20 25 30

Arg Val Met Val Asn Leu Asn Ile Leu Phe  
 40 35 40

45 (2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val  
 1 5 10 15

55 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Pro Pro Leu Ser  
 20 25 30

Thr Phe Thr Ser Asp Phe Tyr Phe Met Glu Phe Gly Ile Glu Val Lys  
 35 40 45

60

692

Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr Lys  
 50 55 60

5 Lys Phe Asn Lys Lys Lys  
 65 70

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

Met Leu Arg Leu Leu Leu Val Ala Phe Ala Leu Val Val Val Leu  
 1 5 10 15

20 Phe His Val Leu Leu Ala Pro Ile Thr Ala Leu Phe His Thr His Phe  
 20 25 30

25 Tyr Asp Arg Leu Gln Asp Ala Gly Ser Arg Trp Pro Glu Leu Tyr Leu  
 35 40 45

Tyr Ser Arg Ala Asp Glu Val Val Leu Ala Arg Asp Ile Glu Arg Met  
 50 55 60

30 Val Glu Ala Arg Leu Ala Arg Arg Val Leu Ala Arg Ser Val Asp Phe  
 65 70 75 80

Val Ser Ser Ala His Val Ser His Leu Arg Asp Tyr Pro Thr Tyr Tyr  
 85 90 95

35 Thr Ser Leu Cys Val Asp Phe Met Arg Asn Cys Val Arg Cys  
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

Met Phe Lys Leu Glu Glu Cys Gly Lys Thr Thr Phe Leu Leu Ser Met  
 1 5 10 15

Ala Leu Tyr Phe Trp Trp Ile Val Gln Thr Thr Lys Gly Cys  
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

5 Met Glu Ser Asp Ala Leu Leu Leu Thr Ile Phe Trp Ile Ile Ala Arg  
 1 5 10 15  
 Ser Ser Val Arg Ser Val Gly Lys Ser Ser Gln Arg Ser Phe Thr Thr  
 20 25 30  
 10 Ile Thr Gln Leu Arg Ser Thr His Thr Gly Pro Ser Arg Arg Ser Tyr  
 35 40 45  
 Leu Ile Trp Trp Asn Gly Gly Pro Lys Arg Thr Ile Ser Tyr Val Ser  
 50 55 60  
 15 Arg Arg Phe Arg Ser Phe Arg  
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

30 Val Gly Leu Phe Gln Pro Lys Thr Phe Gln Val Pro Val Thr Asp Leu  
 1 5 10 15  
 Tyr Ile Phe Ile Lys Ile Tyr Ser Glu Ile Gly Pro Ile Met His Val  
 20 25 30  
 35 Leu Cys Pro Gly Tyr Ser Gln Ser Pro Ser Thr Pro Pro Trp Thr  
 35 40 45

40

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

50 Met Trp Phe Gly Ser Asp Arg Ser Asp Leu Arg Ile Gly Thr Ala Phe  
 1 5 10 15  
 Leu Phe Asp Leu Val Cys Asp Leu Cys Ile His Ala Trp Lys Pro Pro  
 20 25 30  
 55 Gly Leu Val Arg Phe Ser Phe  
 35

60

(2) INFORMATION FOR SEQ ID NO: 585:



## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Leu Asn Thr Ala Ser Leu Asn Leu Pro Trp Lys Val Gln Leu Phe  
1 5 10 15

10 Ala His Ala

## 15 (2) INFORMATION FOR SEQ ID NO: 586:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Ala Cys Leu Leu Leu Phe Leu Ala Phe Ser Trp Lys Arg Lys  
1 5 10 15

25 Gly Leu Trp Ser Gly Pro Gly  
20

30

## (2) INFORMATION FOR SEQ ID NO: 587:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

40 Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser  
1 5 10 15

Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val  
20 25 30

45 Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro  
35 40 45

Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln  
50 55 60

50 Ala His Thr Val Ala  
65

55

## (2) INFORMATION FOR SEQ ID NO: 588:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

60

695

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

5 Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu  
1 5 10 15

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu  
20 25 30

10 Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu  
35 40 45

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr  
50 55 60

15 Arg Lys Lys Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys  
65 70 75

20

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

30 Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe  
1 5 10 15

Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val  
20 25 30

35 Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro  
35 40 45

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala  
50 55 60

40 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro  
65 70 75 80

45 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met  
85 90 95

Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys  
100 105 110

50 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly  
115 120 125

Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys  
130 135 140

55 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa  
145 150 155

60

## (2) INFORMATION FOR SEQ ID NO: 590:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

Met Pro Glu Thr Arg Leu Gly His Arg Gln Gln Phe Ala Val Phe His  
1 5 10 15  
Leu Xaa Pro Val Pro Pro Cys Gly  
20

## (2) INFORMATION FOR SEQ ID NO: 591:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Leu Thr Phe Leu Phe Ser Ala Cys Ala Thr Cys Leu Gly Lys Leu  
1 5 10 15  
Ala Ser Pro Leu Ala Pro Val Gly Pro Gln Gln Arg Gly Xaa Pro Pro  
20 25 30  
Gly Pro Pro Leu Leu Ser  
35

## (2) INFORMATION FOR SEQ ID NO: 592:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

Met Asp Pro Phe His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu  
1 5 10 15  
Val Phe Ala Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser  
20 25 30  
Arg Arg Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp  
35 40 45  
Glu Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro  
50 55 60  
Gln Lys Ala Glu Asn  
65

## (2) INFORMATION FOR SEQ ID NO: 593:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

5  
 10 Asn Leu Arg Val Arg Leu Gly Asp Val Ile Ser Ile Gln Pro Cys Pro  
 1 5 10 15  
 Asp Val Lys Tyr Gly Lys Arg Ile His Val Leu Pro Ile Asp Asp Thr  
 20 25 30  
 15 Val Glu Gly Ile Thr Gly Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr  
 35 40 45  
 Phe Leu Glu Ala Tyr Arg Pro Ile Arg Lys Gly Asp Ile Phe Leu Val  
 50 55 60  
 20 Arg Gly Gly Met Arg Ala Val Glu Phe Lys Val Val Glu Thr Asp Pro  
 65 70 75 80  
 25 Ser Pro Tyr Cys Ile Val Ala Pro Asp Thr Val Ile His Cys Glu Gly  
 85 90 95  
 Glu Pro Ile Lys Arg Glu Asp Glu Glu Glu Ser Leu Asn Glu Val Gly  
 100 105 110  
 30 Tyr Asp Asp Ile Gly Gly Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu  
 115 120 125  
 Met Val Glu Leu Pro Leu Arg His Pro Ala Leu Phe Lys Ala Ile Gly  
 130 135 140  
 35 Val Lys Pro Pro Arg Gly Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly  
 145 150 155 160  
 40 Lys Thr Leu Ile Ala Arg Ala Val Ala Asn Glu Thr Gly Ala Phe Phe  
 165 170 175  
 Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys Leu Ala Gly Glu Ser  
 180 185 190  
 45 Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro  
 195 200 205  
 Ala Ile Ile Phe Ile Asp Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu  
 210 215 220  
 50 Lys Thr His Gly Glu Val Glu Arg Arg Ile Val Ser Gln Leu Leu Thr  
 225 230 235 240  
 55 Leu Met Asp Gly Leu Lys Gln Arg Ala His Val Ile Val Met Ala Ala  
 245 250 255  
 Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg  
 260 265 270  
 60 Phe Asp Arg Glu Val Asp Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu

698

275                      280                      285

Glu Ile Leu Gln Ile His Thr Lys Asn Met Lys Leu Ala Asp Asp Val  
 290                      295                      300

5 Asp Leu Glu Gln  
 305

10

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

15

20

Met Gln Ile Lys Leu Leu Lys Ser Val Lys Thr Val Phe Ala Ile Thr  
 1                      5                      10                      15

Leu Leu Val Leu Phe Leu  
 20

25

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

30

35

Met Phe Pro Lys Phe Cys Pro Ile Leu Ser Leu Val Asp Phe Ile Ser  
 1                      5                      10                      15

His Arg Asp Lys Pro Glu Thr Glu  
 20

40

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

45

50

Met Leu Ile Glu Cys Ala Trp Gln Leu Met Phe Leu Leu Leu Lys Val  
 1                      5                      10                      15

55

Glu Gln Leu Gly Ile Leu Asp Lys  
 20

60

(2) INFORMATION FOR SEQ ID NO: 597:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

Met

1

## (2) INFORMATION FOR SEQ ID NO: 598:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

Met Cys Ile Met Ser Ala Leu Val

1

5

## (2) INFORMATION FOR SEQ ID NO: 599:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

Met Phe Leu Val Trp Phe Phe Trp Gly Leu Ile Ser Ala Leu Ser Asn

1

5

10

15

Val His Thr Pro Ser Arg Leu Pro Ala

20

25

## (2) INFORMATION FOR SEQ ID NO: 600:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

Met Xaa Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser

1

5

10

15

Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly

20

25

## (2) INFORMATION FOR SEQ ID NO: 601:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

700

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

5 Met Trp Thr Arg Ser Ser Arg Cys Leu Leu Leu Cys Ile Pro Gly Xaa  
 1 5 10 15

Ser Arg Arg Arg Arg Ala Gly Ser Gly Met Lys Pro Arg Ser Trp Ser  
 20 25 30

10 Ala Trp Arg Pro Ser Gly Gly Thr Gly Thr Ser Ser Ser Gln Ser Ser  
 35 40 45

15 Thr Gln Ser Arg Thr Leu Ser Ala Thr Ala Ser Pro Ala  
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 602:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu  
 1 5 10 15

30 Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr  
 20 25

(2) INFORMATION FOR SEQ ID NO: 603:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

Met Pro Pro Lys Gln Glu Leu Gly Ser Gly Val Gly Glu Leu Ala Lys  
 1 5 10 15

45 Asn Ser Lys Arg Gln His Trp Asn His Arg Trp Lys Lys Tyr Leu Lys  
 20 25 30

50 Leu Ile Arg Trp Glu Asp Gly Leu Leu Glu Gly Leu Leu Val  
 35 40 45

Leu Glu His Cys Ala Thr Met Ala Trp Asp Cys Leu Met Arg Leu Glu  
 50 55 60

55 Leu Leu Lys Arg Leu  
 65

(2) INFORMATION FOR SEQ ID NO: 604:

60

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

Lys Ile Val Tyr Ile Leu Gly Asn Pro Leu Lys Phe Asn Ser Arg Val  
 1 5 10 15  
 Ile His His Leu Val Leu Leu Gln  
 20

## (2) INFORMATION FOR SEQ ID NO: 605:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

Met Asn Leu His Gln Arg Arg Leu Leu Leu Ile Gly His Leu Met Thr  
 1 5 10 15  
 Leu Val Lys Ala Ser Lys Ser Phe Ser Phe Thr Glu Ile Thr Ser Ser  
 20 25 30  
 Arg Lys Lys  
 35

## (2) INFORMATION FOR SEQ ID NO: 606:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr  
 1 5 10 15  
 Tyr Asn Ile His Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val  
 20 25 30  
 Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr  
 35 40 45  
 Val Gly Pro Thr Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu  
 50 55 60  
 His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Xaa  
 65 70 75 80  
 Glu Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln  
 85 90 95



Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro  
 100 105 110

5 Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln  
 115 120 125

Ser His  
 130

10

(2) INFORMATION FOR SEQ ID NO: 607:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

20 Met Leu Val Ile Phe Leu Phe Thr Ser Leu Leu Lys Ile Pro Ser Ser  
 1 5 10 15

Val Pro Gly Leu Ile Asn Val  
 20

25

(2) INFORMATION FOR SEQ ID NO: 608:

30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

35

Glu Leu Asp Tyr Ile Leu  
 1 5

40

(2) INFORMATION FOR SEQ ID NO: 609:

45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

50 Met Ala Pro Pro Gly Trp Gln Xaa Xaa Xaa Xaa Xaa Trp Leu Ala Cys  
 1 5 10 15

Pro Asp Arg Gly Glu Leu Ser Ser Arg Ser Pro Pro Cys Arg Leu Ala  
 20 25 30

55 Arg Trp Ala Glu Gly Asp Arg Glu Thr Arg Thr Cys Leu Leu Glu Leu  
 35 40 45

Ser Ala Gln Ser Trp Gly Gly Arg Phe Arg Arg Ser Ser Ala Val Ser  
 50 55 60

60

703

Ala Gly Ser Pro Ser Arg Leu His Phe Leu Pro Gln Pro Leu Leu Leu  
65 70 75 80

5 Arg Ser Ser Gly Ile Pro Ala Ala Ala Thr Pro Trp Pro Gln Pro Ala  
85 90 95

Gly Leu Pro Val Arg Pro Thr Pro Thr Arg Thr Gly Glu Glu Asp Arg  
100 105 110

10 Thr Leu Asp Ile Ser Ile Cys Thr Glu Val Leu Ala Gly Thr Glu Gln  
115 120 125

Pro Pro Pro Pro Arg Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg  
130 135 140

15 Leu Glu Thr Leu Asp Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg  
145 150 155 160

20 Gly Lys Leu Asp Phe Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe  
165 170 175

Gln Gly Glu Asp Arg Lys Phe Ala Pro Ser Asp Lys Ser Gln Pro Pro  
180 185 190

25 Thr Thr Glu Arg Glu Gln Val Pro Val Ser Arg Ile Gln Thr Asp Leu  
195 200 205

Thr Glu Ile Gly Ser Ser Met Arg Ser Pro Gly Val Ser Pro Arg Ile  
210 215 220

30 Trp Leu Asp Phe Gln Ser Thr Xaa  
225 230

35

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

45

Met Val Leu Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu  
1 5 10 15

Leu Leu Asn Met Leu Ile Ala Leu Met Xaa Arg Asp Arg Gln Gln Cys  
20 25 30

50

Arg His

55

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

Met Val Phe Glu Gly Phe Ser Ser Ala Phe Cys Leu Ser Ser Thr Ala  
 1 5 10 15  
 Pro Thr Ser His Pro  
 20

10

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

Gly Lys Lys Asn Gln Leu Leu Val Ile  
 1 5  
 20

25

(2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val  
 1 5 10 15

35

Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys  
 20 25

40

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

Met Ala Lys Arg Ser Pro Gly Gly Cys Gly Ser Gly Leu Ile Leu Leu  
 1 5 10 15

50

Cys Cys Gln Pro Cys Arg Pro Thr Ser Ser Ala Pro Met Arg  
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

5     Ile Thr Ile Ala Ile Gln Met Ile Cys Leu Val Asn Xaa Glu Leu Tyr  
       1                   5                   10                   15  
       Pro Thr Phe Val Arg Asn Xaa Gly Val Met Val Cys Ser Ser Leu Cys  
           20                   25                   30  
 10    Asp Ile Gly Gly Ile Ile Thr Pro Phe Ile Val Phe Arg Leu Arg Glu  
           35                   40                   45  
       Val Trp Gln Ala Leu Pro Leu Ile Leu Phe Ala Val Leu Gly Leu Leu  
           50                   55                   60  
 15    Ala Ala Gly Val Thr Leu Leu Leu Pro Glu Thr Lys Gly Val Ala Leu  
           65                   70                   75                   80  
       Pro Glu Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys Pro  
           85                   90                   95  
       Lys Glu Asn Thr Ile Tyr Leu Lys Val Gln Thr Ser Glu Pro Ser Gly  
           100                   105                   110  
 25    Thr

30    (2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

35     Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys Pro Lys Glu  
       1                   5                   10                   15  
 40    Asn Thr

45    (2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

50     Pro Arg Val Arg Asn Ser Pro Glu Asp Leu Gly Leu Ser Leu Thr Gly  
       1                   5                   10                   15  
       Asp Ser Cys Lys Leu  
           20  
 60

## 5

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 618:

15

Gly Gly Gly Pro Trp Ala Gly Ser Trp Leu Ser Pro Lys Thr Pro Gly  
20 25 30

Ala Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg  
35 40 45

20            Lys Arg Leu Leu  
                 50

(2) INFORMATION FOR SEQ ID NO: 619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(D). TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu Ala Xaa Xaa  
1 5 10 15

35 Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp Phe Gly Gly  
20 25 30

Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr Leu Trp Leu  
35 40 45

40 Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val Val Pro Gly  
50 55 60

	Thr	Met	Trp	Gly	Lys	Ile	Val	Cys	Leu	Cys	Thr	Gly	Val	Met	Gly	Val
45	65					70					75					80

Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys Leu Glu Phe  
85 90 95

50 Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Ile Gln Tyr  
100 105 110

Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln Glu Ala Trp  
115 120 125

Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala Ala Arg Xaa  
130 135 140

60 His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg Gln Val Arg  
145 150 155 160

707

Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser Met Val Asp Ile  
 165 170 175

5 Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln Asn Leu Ser Ser  
 180 185 190

Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu Ala Gly Lys Leu  
 195 200 205

10 Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly Pro Arg Gln Leu  
 210 215 220

15 Pro Glu Pro Ser Gln Gln Ser Lys  
 225 230

(2) INFORMATION FOR SEQ ID NO: 620:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly  
 1 5 10 15

30 Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser  
 20 25 30

Gly Ala Gly Lys  
 35

35

(2) INFORMATION FOR SEQ ID NO: 621:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

45

Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu  
 1 5 10 15

50 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser  
 20 25 30

Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala  
 35 40 45

55 His Lys Ala Lys Ser His Pro Glu Val  
 50 55

60 (2) INFORMATION FOR SEQ ID NO: 622:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln  
1 5 10 15

Pro Ser Asp

## (2) INFORMATION FOR SEQ ID NO: 623:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

Asn Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser  
1 5 10 15

Lys Ser Tyr

## (2) INFORMATION FOR SEQ ID NO: 624:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys Ile Phe  
1 5 10 15

Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met Asn Ser  
20 25 30

Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser Asp Ser  
35 40 45

Ala Gly Pro  
50

## (2) INFORMATION FOR SEQ ID NO: 625:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

Ile Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala  
1 5 10 15

5 His Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys  
20 25 30

Lys Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu  
35 40 45

10 Gln Lys Gln Leu Leu Arg His Ala Lys His His Thr  
50 55 60

15

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

20 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

25 Asp Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser  
1 5 10 15

Ser His Asn Leu Ala Val His Arg Met Ile His Thr Gly Glu Lys  
20 25 30

30

(2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

40 Arg Ser Ser Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile Cys Lys Ser  
1 5 10 15

Glu Pro Asn Thr Asp Gln Leu Asp Tyr  
20 25

45

(2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

55

Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu  
1 5 10 15

60 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser  
20 25 30



710

Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala  
           35                          40                          45  
 5 His Lys Ala Lys Ser His Pro Glu Val Xaa Ile Thr Ser Thr Asp Ile  
           50                          55                          60  
 Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln Pro Ser Asp Xaa Asn Ser  
           65                          70                          75                          80  
 10 Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser Lys Ser  
                           85                          90                          95  
 Tyr Xaa Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys  
                           100                          105                          110  
 15 Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met  
           115                          120                          125  
 20 Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser  
           130                          135                          140  
 Asp Ser Ala Gly Pro Xaa Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala  
           145                          150                          155                          160  
 25 Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met Ile His  
                           165                          170                          175  
 30 Thr Gly Glu Lys His Tyr Xaa  
           180

(2) INFORMATION FOR SEQ ID NO: 629:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His  
           1                          5                          10                          15  
 45 Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys  
           20                          25                          30  
 Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln  
           35                          40                          45  
 50 Lys Gln Leu Leu Arg His Ala Lys His His Thr Asp  
           50                          55                          60

55

(2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

60

711

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

5 Pro Phe Lys Asp Asp Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu  
 1 5 10 15  
 Arg Glu Thr Pro Lys Pro Arg Arg Lys Ser Gly  
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

20 Glu Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu  
 1 5 10 15  
 Met Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val  
 20 25 30  
 25 Leu Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu  
 35 40 45  
 30 Trp Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg  
 50 55 60  
 Met Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val  
 65 70 75 80  
 35 Gln Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu  
 85 90 95  
 Asn Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met  
 100 105 110  
 40

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

50 Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg Pro Thr Gly Gln Gln  
 1 5 10 15  
 55 Leu Glu Ser Leu Gly Leu Leu Ala  
 20

60

(2) INFORMATION FOR SEQ ID NO: 633:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

Val His Arg Glu Glu Ala Ser Cys Tyr Cys Gln Ala Glu Pro Ser Gly  
 1 5 10 15

10 Asp Leu

## 15 (2) INFORMATION FOR SEQ ID NO: 634:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

Arg Pro Ala Leu Arg Gln Ala Gly Gly Gly Thr Arg Glu Pro Arg Gln  
 1 5 10 15

25 Lys Arg Trp Ala Gly Leu  
 20

## 30 (2) INFORMATION FOR SEQ ID NO: 635:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

40 Ala Val Asn Phe Arg Pro Gln Arg Ser Gln Ser Met  
 1 5 10

## 45 (2) INFORMATION FOR SEQ ID NO: 636:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met Leu Gly Val  
 1 5 10 15

55 Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val Ala Val Asn Asn  
 20 25 30

Pro Lys Lys Gln Glu  
 35

60

## (2) INFORMATION FOR SEQ ID NO: 637:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

10

Glu Glu Met Ala Asp Ser Val Lys Thr Phe Leu Gln Asp Leu Ala Arg  
 1 5 10 15

15

Gly Ile Lys Asp Ser Ile Trp Gly Ile Cys Thr Ile Ser Lys Leu Asp  
 20 25 30

Ala Arg Ile Gln Gln Lys Arg Glu Glu Gln Arg Arg Arg Ala Ser  
 35 40 45

20

Ser Val Leu Ala Gln Arg Arg Ala Gln Ser Ile Glu Arg Lys Gln Glu  
 50 55 60

25

Ser Glu Pro Arg Ile Val Ser Arg Ile Phe Gln Cys Cys Ala Trp Asn  
 65 70 75 80

Gly Gly Val Phe Trp Phe Ser Leu Leu Leu Phe Tyr Arg Val Phe Ile  
 85 90 95

30

Pro Val Leu Gln Ser Val Thr Ala Arg Ile Ile Gly Asp Pro Ser Leu  
 100 105 110

His Gly Asp Val Trp Ser Trp Leu Glu Phe Phe Leu Thr Ser Ile Phe  
 115 120 125

35

Ser Ala Leu Trp Val Leu Pro Leu Phe Val Leu Ser Lys Val Val Asn  
 130 135 140

40

Ala Ile Trp Phe Gln Asp Ile Ala Asp Leu Ala Phe Glu Val Ser Gly  
 145 150 155 160

Arg Lys Pro His Pro Phe Pro Ser Val Ser Lys Ile Ile Ala Asp Met  
 165 170 175

45

Leu Phe Asn Leu Leu Leu Gln Ala Leu Phe Leu Ile Gln Gly Met Phe  
 180 185 190

Val Ser Leu Phe Pro Ile His Leu Val Gly Gln Leu Val Ser Leu Leu  
 195 200 205

50

His Met Ser Leu Leu Tyr Ser Leu Tyr Cys Phe Glu Tyr Arg Trp Phe  
 210 215 220

55

Asn Lys Gly Ile Glu Met His Gln Arg Leu Ser Asn Ile Glu Arg Asn  
 225 230 235 240

Trp Pro Tyr Tyr Phe Gly Phe Gly Leu Pro Leu Ala Phe Leu Thr Ala  
 245 250 255

60

Met Gln Ser Ser Tyr Ile Ile Ser Gly Cys Leu Phe Ser Ile Leu Phe  
 260 265 270

Pro Leu Phe Ile Ile Ser Ala Asn Glu Ala Lys Thr Pro Gly Lys Ala  
 275 280 285

5 Tyr Leu Phe Gln Leu Arg Leu Phe Ser Leu Val Val Phe Leu Ser Asn  
 290 295 300

Arg Leu Phe His Lys Thr Val Tyr Leu Gln Ser Ala Leu Ser Ser Ser  
 305 310 315 320

10 Thr Ser Ala Glu Lys Phe Pro Ser Pro His Pro Ser Pro Ala Lys Leu  
 325 330 335

Lys Ala Thr Ala Gly His  
 340

15

## (2) INFORMATION FOR SEQ ID NO: 638:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

Met Ala Lys Phe Met Thr Pro Val Ile Gln Asp Asn Pro Ser Gly Trp  
 1 5 10 15

30 Gly Pro Cys Ala Val Pro Glu Gln Phe Arg Asp Met Pro Tyr Gln Pro  
 20 25 30

Phe Ser Lys Gly Asp Arg Leu Gly Lys Val Ala Asp Trp Thr Gly Ala  
 35 40 45

35 Thr Tyr Gln Asp Lys Arg Tyr Thr Asn Lys Tyr Ser Ser Gln Phe Gly  
 50 55 60

40 Gly Gly Ser Gln Tyr Ala Tyr Phe His Glu Glu Asp Glu Ser Ser Phe  
 65 70 75 80

Gln Leu Val Asp Thr Ala Arg Thr Gln Lys Thr Ala Tyr Gln Arg Asn  
 85 90 95

45 Arg Met Arg Phe Ala Gln Arg Asn Leu Arg Arg Asp Lys Asp Arg Arg  
 100 105 110

Asn Met Leu Gln Phe Asn Leu Gln Ile Leu Pro Lys Ser Ala Lys Gln  
 115 120 125

50 Lys Glu Arg Glu Arg Ile Arg Leu Gln Lys Lys Phe Gln Lys Gln Phe  
 130 135 140

55 Gly Val Arg Gln Lys Trp Asp Gln Lys Ser Gln Lys Pro Arg Asp Ser  
 145 150 155 160

Ser Val Glu Val Arg Ser Asp Trp Glu Val Lys Glu Glu Met Asp Phe  
 165 170 175

60 Pro Gln Leu Met Lys Met Arg Tyr Leu Glu Val Ser Glu Pro Gln Asp

715

	180	185	190
	Ile Glu Cys Cys Gly Ala Leu Glu Tyr Tyr Asp Lys Ala Phe Asp Arg		
	195	200	205
5	Ile Thr Thr Arg Ser Glu Lys Pro Leu Arg Xaa Xaa Lys Arg Ile Phe		
	210	215	220
10	His Thr Val Thr Thr Thr Asp Asp Pro Val Ile Arg Lys Leu Ala Lys		
	225	230	235 240
	Thr Gln Gly Asn Val Phe Ala Thr Asp Ala Ile Leu Ala Thr Leu Met		
	245	250	255
15	Ser Cys Thr Arg Ser Val Tyr Ser Trp Asp Ile Val Val Gln Arg Val		
	260	265	270
	Gly Ser Lys Leu Phe Phe Asp Lys Arg Asp Asn Ser Asp Phe Asp Leu		
	275	280	285
20	Leu Thr Val Ser Glu Thr Ala Asn Glu Pro Pro Gln Asp Glu Gly Asn		
	290	295	300
	Ser Phe Asn Ser Pro Arg Asn Leu Ala Met Glu Ala Thr Tyr Ile Asn		
	305	310	315 320
25	His Asn Phe Ser Gln Gln Cys Leu Arg Met Gly Lys Glu Arg Tyr Asn		
	325	330	335
30	Phe Pro Asn Pro Asn Pro Phe Val Glu Asp Asp Met Asp Lys Asn Glu		
	340	345	350
	Ile Ala Ser Val Ala Tyr Arg Tyr Arg Ser Gly Lys Leu Gly Asp Asp		
	355	360	365
35	Ile Asp Leu Ile Val Arg Cys Glu His Asp Gly Val Met Thr Gly Ala		
	370	375	380
40	Asn Gly Glu Val Ser Phe Ile Asn Ile Lys Thr Leu Asn Glu Trp Asp		
	385	390	395 400
	Ser Arg His Cys Asn Gly Val Asp Trp Arg Gln Lys Leu Asp Ser Gln		
	405	410	415
45	Arg Gly Ala Val Ile Ala Thr Glu Leu Lys Asn Asn Ser Tyr Lys Leu		
	420	425	430
	Ala Arg Trp Thr Cys Cys Ala Leu Leu Ala Gly Ser Glu Tyr Leu Lys		
	435	440	445
50	Leu Gly Tyr Val Ser Arg Tyr His Val Lys Asp Ser Ser Arg His Val		
	450	455	460
55	Ile Leu Gly Thr Gln Gln Phe Lys Pro Asn Glu Phe Ala Ser Gln Ile		
	465	470	475 480
	Asn Leu Ser Val Glu Asn Ala Trp Gly Ile Leu Arg Cys Val Ile Asp		
	485	490	495
60	Ile Cys Met Lys Leu Glu Glu Gly Lys Tyr Leu Ile Leu Lys Asp Pro		

500                      505                      510

Asn Lys Gln Val Ile Arg Val Tyr Ser Leu Pro Asp Gly Thr Phe Ser  
 515                      520                      525

5 Ser

10

(2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

20 Lys Lys Arg His Thr Asp Val Gln Phe Tyr Thr Glu Val Gly Glu Ile  
 1                      5                      10                      15

Thr Thr Asp Leu Gly Lys His Gln His Met His Asp Arg Asp Asp Leu  
                     20                      25                      30

25 Tyr Ala Glu Gln Met Glu Arg Glu Met Arg His Lys Leu Lys Thr Ala  
                     35                      40                      45

Phe Lys Asn Phe Ile Glu Lys Val Glu Ala Leu Thr Lys Glu Glu Leu  
                     50                      55                      60

30 Glu Phe Glu Val Pro Phe Arg Asp Leu Gly Phe Asn Gly Ala Pro Tyr  
                     65                      70                      75                      80

35 Arg Ser Thr Cys Leu Leu Gln Pro Thr Ser Ser Ala Leu Val Asn Ala  
                     85                      90                      95

Thr Glu Trp Pro Pro Phe Val Val Thr Leu Asp Glu Val Glu Leu Ile  
                     100                      105                      110

40 His Phe Xaa Arg Val Gln Phe His Leu Lys Asn Phe Asp Met Val Ile  
                     115                      120                      125

Val Tyr Lys Asp Tyr Ser Lys Lys Val Thr Met Ile Asn Ala Ile Pro  
                     130                      135                      140

45 Val Ala Ser Leu Asp Pro Ile Lys Glu Trp Leu Asn Ser Cys Asp Leu  
                     145                      150                      155                      160

50 Lys Tyr Thr Glu Gly Val Gln Ser Leu Asn Trp Thr Lys Ile Met Lys  
                     165                      170                      175

Thr Ile Val Asp Asp Pro Glu Gly Phe Phe Glu Gln Gly Gly Trp Ser  
                     180                      185                      190

55 Phe Leu

60

(2) INFORMATION FOR SEQ ID NO: 640:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

Arg Ser Gly Leu Gly Leu Gly Ile Thr Ile Ala Phe Leu Ala Thr Leu  
1 5 10 15  
Ile Thr Gln Phe Leu Val Tyr Asn Gly Val Tyr Gln Tyr Thr Ser Pro  
20 25 30  
Asp Phe Leu Tyr Ile Arg Ser Trp Leu Pro Cys Ile Phe Phe Ser Gly  
35 40 45  
Gly Val Thr Val Gly Asn Ile Gly Arg Gln Leu Ala Met Gly Val Pro  
50 55 60  
Glu Lys Pro His Ser Asp  
65 70

## (2) INFORMATION FOR SEQ ID NO: 641:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser Val Glu  
1 5 10 15  
Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Xaa Xaa Pro Xaa  
20 25 30  
Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr  
35 40 45  
Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe  
50 55 60  
Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile Ser Asn  
65 70 75 80  
Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp  
85 90 95  
Thr Arg Arg Ser Gly  
100

## (2) INFORMATION FOR SEQ ID NO: 642:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

5 Met Glu Ala Gln Gln Val Asn Glu Ala Glu Ser Ala Arg Glu Gln Leu  
 1 5 10 15  
 Gln Xaa Leu His Asp Gln Ile Ala Gly Gln Lys Ala Ser Lys Gln Glu  
 20 25 30  
 10 Leu Glu Thr Glu Leu Glu Arg Leu Lys Gln Glu Phe His Tyr Ile Glu  
 35 40 45  
 Glu Asp Leu Tyr Arg Thr Lys Asn Thr Leu Gln Ser Arg Ile Lys Asp  
 50 55 60  
 15 Arg Asp Glu Glu Ile Gln Lys Leu Arg Asn Gln Leu Thr Asn Lys Thr  
 65 70 75 80  
 Leu Ser Asn Ser Ser Gln Ser Glu Leu Glu Asn Arg Leu His Gln Leu  
 85 90 95  
 Thr Glu Thr Leu Ile Gln Lys Gln Thr Met Leu Glu Ser Leu Ser Thr  
 100 105 110  
 25 Glu Lys Asn Ser Leu Val Phe Gln Leu Glu Arg Leu Glu Gln Gln Met  
 115 120 125  
 Asn Ser Ala Ser Gly Ser Ser Ser Asn Gly Ser Ser Ile Asn Met Ser  
 130 135 140  
 30 Gly Ile Asp Asn Gly Glu Gly Thr Arg Leu Arg Asn Val Pro Val Leu  
 145 150 155 160  
 Phe Asn Asp Thr Glu Thr Asn Leu Ala Gly Met Tyr Gly Lys Val Arg  
 165 170 175  
 Lys Ala Ala Ser Ser Ile Asp Gln Phe Ser Ile Arg Leu Gly Ile Phe  
 180 185 190  
 40 Leu Arg Arg Tyr Pro Ile Ala Arg Val Phe Val Ile Ile Tyr Met Ala  
 195 200 205  
 Leu Leu His Leu Trp Val Met Ile Val Leu Leu Thr Tyr Thr Pro Glu  
 210 215 220  
 45 Met His His Asp Gln Pro Tyr Gly Lys  
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

60 Ile Arg His Glu Gln His Pro Asn Phe Ser Leu Glu Met His Ser Lys  
 1 5 10 15

Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile Leu Ile Leu Pro  
20 25 30

5 Val Cys Ala His Leu His Glu Glu Leu Asn Cys  
35 40

10 (2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

Ser Phe Phe Ile Ser Glu Glu Lys Gly His Leu Leu Leu Gln Ala Glu  
1 5 10 15

20 Arg His Pro Trp Val Ala Gly Ala Leu Val Gly Val Ser Gly Gly Leu  
20 25 30

25 Thr Leu Thr Thr Cys Ser Gly Pro Thr Glu Lys Pro Ala Thr Lys Asn  
35 40 45

Tyr Phe Leu Lys Arg Leu Leu Gln Glu Met His Ile Arg Ala Asn  
50 55 60

30

35

## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    February 26, 1997	Accession Number    97897
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A. The indications made below relate to the microorganism referred to in the description</b> on page <u>116</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    May 15, 1997	Accession Number    209043
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>119</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    September 4, 1997	Accession Number    209235
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>12301 Parklawn Drive Rockville, Maryland 20852 United States of America</p>	
Date of deposit <u>February 26, 1997</u>	Accession Number <u>97898</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>May 15, 1997</u>	Accession Number <u>209044</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")          	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    February 26, 1997	Accession Number    97899
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit <u>May 15, 1997</u>	Accession Number <u>209045</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>130</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit April 28, 1997	Accession Number 209011
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    February 26, 1997	Accession Number    97900
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97901
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    May 15, 1997	Accession Number    209046
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    May 15, 1997	Accession Number    209047
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (If the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) <p>12301 Parklawn Drive Rockville, Maryland 20852 United States of America</p>	
Date of deposit    May 22, 1997	Accession Number    209076
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<p style="text-align: center;">For receiving Office use only</p> <div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px;">Authorized officer <p style="text-align: center;"><b>Susan White</b> PCT International Division</p></div>	<p style="text-align: center;">For International Bureau use only</p> <div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px;">Authorized officer</div>
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>140</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 .. United States of America	
Date of deposit August 21, 1997	Accession Number 209215
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    February 26, 1997	Accession Number    97904
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>154</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="margin-left: 100px;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) <div style="margin-left: 10px;">12301 Parklawn Drive Rockville, Maryland 20852 United States of America</div>	
Date of deposit    July 3, 1997	Accession Number    209139
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer    <b>Susan White</b> PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    May 15, 1997	Accession Number    209049
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (If the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" style="margin-right: 10px;" type="checkbox"/><div>This sheet was received with the international application</div></div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input style="margin-right: 10px;" type="checkbox"/><div>This sheet was received by the International Bureau on:</div></div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    February 26, 1997	Accession Number    97903
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    June 12, 1997	Accession Number    209119
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;"><b>Susan White</b> PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    February 26, 1997	Accession Number    97902
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; text-align: center;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer    <b>Susan White</b>                                  <b>PCT International Division</b></div>	<div style="border-bottom: 1px solid black; text-align: center;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT <span style="float: right;">Further deposits are identified on an additional sheet <input type="checkbox"/></span>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit <u>May 15, 1997</u>	Accession Number <u>209048</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit    May 15, 1997	Accession Number    209050
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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## INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

<b>A.</b> The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
<b>B. IDENTIFICATION OF DEPOSIT</b> <span style="float: right;">Further deposits are identified on an additional sheet <input checked="" type="checkbox"/></span>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 12, 1998</u>	Accession Number <u>209627</u>
<b>C. ADDITIONAL INDICATIONS</b> (leave blank if not applicable) <span style="float: right;">This information is continued on an additional sheet <input type="checkbox"/></span>	
<b>D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE</b> (if the indications are not for all designated States)	
<b>E. SEPARATE FURNISHING OF INDICATIONS</b> (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<b>For receiving Office use only</b>  <input checked="" type="checkbox"/> This sheet was received with the international application  Authorized officer <u>Susan White</u> <u>PCT International Division</u>	<b>For International Bureau use only</b>  <input type="checkbox"/> This sheet was received by the International Bureau on:  Authorized officer _____
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***What Is Claimed Is:***

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group  
5 consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

10 (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

15 (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X,  
20 having biological activity;

(f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

25 (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the  
30 polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included  
35 in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

10

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

15

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

20

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

25

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

30

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

35

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

5 12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

10 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15 15. A method of making an isolated polypeptide comprising:  
15 (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and  
(b) recovering said polypeptide.

20 16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

25 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and  
(b) diagnosing a pathological condition or a susceptibility to a pathological  
30 condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of  
35 claim 11 in a biological sample; and  
(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- 5 (a) contacting the polypeptide of claim 11 with a binding partner; and  
(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

10 22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;  
(b) isolating the supernatant;  
(c) detecting an activity in a biological assay; and  
15 (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.